BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

THE JOURNAL OF BIOLOGICAL CHEMISTRY
Vol. 267, No. 13, Issue of May 5, pp. 9101-9106, 1992
Printed in U.S.A.

The Human Leukocyte Platelet-activating Factor Receptor

cDNA CLONING, CELL SURFACE EXPRESSION, AND CONSTRUCTION OF A NOVEL EPITOPE-BEARING ANALOG*

(Received for publication, June 12, 1991, and in revised form, October 14, 1991)

Dieter Kunz‡, Norma P. Gerard§, and Craig Gerard§¶

From the Department of Pediatrics and the Ina Sue Perlmutter Laboratory, Children's Hospital, the Department of Medicine, Beth Israel Hospital, and the Thorndike Laboratory, Harvard Medical School, Boston, Massachusetts 02115

A human myeloid transcript of approximately 4 kilobases was cloned as a cDNA from an expression library based on homology with the guinea pig cDNA recently described by Honda *et al.* (Honda, Z-I., Nakamura, M., Miki, I., Minami, M., Watanabe, T., Seyama, Y., Okado, H., Tok, H., Ito, K., Miyamato, T., and Shimizu, T. (1991) *Nature* 349, 342–346) as a receptor for platelet-activating factor (PAF). The cloned DNA confers high affinity binding sites for platelet-activating factor when transfected into COS-7 cells and has binding and desensitization properties similar to the human leukocyte receptor. Southern analysis using this cDNA indicates that the PAF receptor gene is present as a single copy in the human genome. The deduced protein sequence predicts seven hydrophobic regions for the PAF receptor, characteristic of the rhodopsin gene family, and is 83% identical to the deduced protein sequence of the corresponding guinea pig molecule. A modified human PAF receptor cDNA was constructed by inserting an additional 30 nucleotides after the 5′-ATG, encoding the amino acid sequence MDYKDDDDKEF, which is specifically recognized by a monoclonal antibody. The modified cDNA encodes a functional PAF receptor and is detected by antibody on the membrane of transfected COS-7 cells. The use of this construct supports the structural model for the rhodopsin-like superfamily of receptors which places the NH_2-terminal sequence on the extracellular side of the membrane, and should additionally be useful for affinity purification of the receptor protein.

The phospholipid, platelet-activating factor (PAF),[1] displays a wide variety of biological functions *in vivo*, including granulocyte activation and chemotaxis, platelet activation, enhancement of vascular permeability, smooth muscle contraction, bronchospasm, and hypotension (1–4). These anaphylactoid actions occur in response to nanomolar quantities of PAF, and are mediated by specific receptors which are pharmacologically coupled to GTP-binding proteins (5–7). Pharmacologic studies with antagonist compounds and binding parameters suggest that there may be multiple receptors for PAF (8, 9).

Platelet-activating factor is known to be made up of a complex group of structurally related phospholipids characterized by an ether linkage at the *sn*-1 position, an acetyl moiety at *sn*-2 and a choline head group at *sn*-3 (10–12). Variations in the alkyl chain length have been observed or synthesized at both the 1 and 2 positions, and there are stereospecific requirements for biological function as well. No pharmacologic subclassification of PAF receptors has arisen from structure-activity studies with PAF analogs.

Recently Honda *et al.* (13), reported the molecular cloning of a guinea pig lung receptor for PAF identified by expression in *Xenopus* oocytes. Because of questions arising in the human system relating to the number and identity of PAF receptor(s), we screened a U937 myeloid cell expression library using a probe prepared from guinea pig lung cDNA. In this article, we report the cloning and expression of a high affinity human receptor for PAF, and present immunohistochemical data on the topology of the receptor in transfected cell membranes.

EXPERIMENTAL PROCEDURES

Materials—Reagents and enzymes used in the construction of cDNA were products of Boehringer Mannheim. pCDM8 vector and *Escherichia coli* MC1061/p3 were the gift of Dr. Brian Seed, Harvard Medical School. PCR reagents and the thermal cycler were products of Perkin-Elmer Cetus. WEB2086 was provided by Boehringer Ingleheim. COS-7 cells were obtained from the American Type Culture Association. [^{3}H]Hexadecyl-PAF (60 Ci/mmol) was obtained from Du Pont-New England Nuclear. Northern and Southern hybridizations were performed with GeneScreen *Plus* membranes using protocols recommended by Du Pont-New England Nuclear. Anti-Flag M5 antibody was a generous gift from Immunex. Peroxidase-labeled anti-mouse IgG was a product of Vector Laboratories.

Molecular Cloning of a Myeloid PAF Receptor—Oligonucleotides corresponding to the 5′- and 3′-coding sequences for the guinea pig PAF receptor were prepared containing *Bam*HI sites (5′-CCGGATC CGAGCCATGGAGTTAAACAGA-3′, sense; 5′-CCGGATCCAGCA AGCAGGAACTAATT-3′, antisense). Guinea pig lung total RNA (2 μg) (14) was reverse transcribed with 20 units of avian myeloblastosis virus reverse transcriptase and 1 μg of oligo(dT) primer (15). This mixture was next added to a PCR reaction mixture containing 1 μM each of the sense and antisense primers described above, according to the recommendations provided with AmpliTaq DNA polymerase. Five cycles of PCR were performed with oligonucleotide hybridization at 45 °C, and 30 subsequent cycles performed at 55 °C. The band at approximately 1 kb was isolated following agarose gel electrophoresis

* This work was supported by National Institutes of Health Grant HL 36162. While this manuscript was in review, Nakamura *et al.* (34) and Ye *et al.* (35) also reported cDNA sequences for the human PAF receptor. The sequences reported are identical to the one reported herein, with the exception of a T → C substitution at nucleotide 471 which makes no change in the amino acid. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "*advertisement*" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

The nucleotide sequence(s) reported in this paper has been submitted to the GenBank™/EMBL Data Bank with accession number(s) M76674.

‡ Current address: Dept. of Pharmacology, Biocenter of the University of Basel, Klingelbergstrasse 70, CH-4056 Basel, Switzerland.

§ To whom correspondence should be addressed: Pulmonary Div., Dept. of the Pediatrics, Children's Hospital, 320 Longwood Ave., Boston, MA 02115. Tel.: 617-735-6174; Fax: 617-730-0422.

¶ Recipient of a Faculty Scholar's Award from R. J. R. Nabisco.

[1] The abbreviations used are: PAF, platelet-activating factor; kb, kilobase; PCR, polymerase chain reaction.

of a portion of the reaction mixture (GeneClean, Bio101, La Jolla, CA), and was labeled using random primers and [^{32}P]dCTP. This probe was used to screen a U937 cDNA library constructed in the expression vector pCDM8 as previously described (16). The colonies were hybridized under conditions of low stringency using 25% formamide, 5 × SSC, 1 × Denhardt's solution, and 0.1% sodium pyrophosphate at 37 °C for 18 h. Filters were washed in 2 × SSC at room temperature for 30 min with three exchanges and autoradiograms exposed for 24 h at −70 °C using an image intensifying screen. Positively hybridizing colonies in the primary library were purified and characterized. A clone, CS1, was identified by sequence analysis to contain a full length coding sequence with significant similarities to the guinea pig lung PAF receptor cDNA. This clone was extensively sequenced on both strands using the dideoxy technique with double stranded template (17). Several partial length clones were also characterized from an HL60 cell library (generous gift of Dr. Stuart Orkin, Harvard Medical School), and these sequences all yielded an unambiguous structure.

Genomic DNA and RNA Analyses—Genomic DNA was prepared from peripheral blood leukocytes (18) and 7.5-μg aliquots were digested with restriction enzymes in 20-μl aliquots overnight at 37 °C. Samples were electrophoresed at 5 V/cm through 0.9% agarose gels in 1 × TAE (Tris acetate/EDTA) buffer and blotted to GeneScreen *Plus* membranes by capillary action according to the manufacturer's instructions. Hybridization was performed in 50% formamide at 42 °C overnight using 10^6 cpm/ml of [^{32}P]dCTP-labeled insert of clone CS1. Final washing conditions were 0.2 × SSC and room temperature for 30 min. Autoradiographs were prepared using an image intensifying screen for 24 h at −70 °C. Polyadenylated RNA was prepared with oligo(dT)-cellulose (Collaborative Research, Bedford, MA) (19) using RNA from undifferentiated U937 cells, from U937 cells differentiated for 72 h with 1 mM dibutyryl-cAMP, or from bronchiectatic human lung parenchyma resected from a patient with cystic fibrosis. Samples of 2 μg were denatured using formaldehyde and electrophoresed through 0.9% agarose. Transfer to GeneScreen *Plus* membranes, hybridization, and washing were accomplished as described above. Autoradiographs were prepared using an image intensifying screen at −70 °C for 7 days.

Construction of Flag-PAF Receptor cDNA—The Flag/pCDM8 construct was created to allow COS cell expression of Flag fusion proteins (20). A synthetic duplex oligonucleotide, 5′-AGCTTCCA GCA GCC ATG GAC TAC AAG GAC GAC GAT GAC AAA GAATTC-3′, bearing a *Hin*dIII site and an *Eco*RI site, was ligaaed to a modified pCDM8 vector containing a pBluescript polylinker. The oligonucleotide bears the consensus sequence corresponding to the human NK-2 receptor (21) 5′ to the ATG at position 15, which subsequently encodes the Flag sequence, MDYKDDDDKEF. An insert encoding the human PAF receptor was prepared by PCR using a primer which mutated the normal initiating methionine to a leucine (ATG → CTG), placing the PAF receptor sequence downstream from the initiating methionine ATG for the Flag sequence.

COS Cell Expression of the Human Myeloid PAF Receptor—COS-7 cells were plated at a density of 10^6 cells/10-cm dish following trypsinization, and were grown for 18–24 h in Dulbecco's modified Eagle's medium supplemented with nonessential amino acids, sodium pyruvate, 6 mM glutamine, and 10% fetal calf serum. Cells were transfected with 2 μg of plasmid in 3 ml of Dulbecco's modified Eagle's medium containing 10% NuSerum (Collaborative Research), 1 mM chloroquine (freshly prepared, Sigma), and 400 μg/ml of DEAE-dextran (Sigma). Transfections were incubated at 37 °C in an atmosphere of 5% CO_2 in air for 2.5–3 h. The cells were then shocked with 10% dimethyl sulfoxide in phosphate-buffered saline for 5–10 min at room temperature and returned to media containing 10% fetal calf serum. 72–90 h following transfection the cells were washed with binding buffer consisting of 0.15 M choline chloride, 10 mM Tris-HCl, pH 7.5, 10 mM $MgCl_2$, and 0.25% bovine serum albumin, and incubated in the same buffer with 2 nM ^{3}H-labeled PAF and appropriate concentrations of unlabeled PAF or WEB2086 for 30 min at 4 or 22 °C. Uptake of radiolabeled ligand as a function of time was determined at 4 °C. Desensitization of binding was performed by preincubating transfected cells with increasing concentrations of unlabeled PAF for 20 min at 4 °C, washing, and subsequently incubating with 2 nM ^{3}H-labeled PAF for 30 min at 4 °C. Cells were washed with binding buffer, solubilized with 0.5% Triton X-100, scraped into scintillation vials, and cell-associated ligand determined by scintillation counting. Nonspecific binding was determined in the presence of 10 μM unlabeled PAF. The K_d was determined from Scatchard analysis of the data obtained from duplicate points and three separate transfection experiments.

Immunohistochemical Staining of Flag-PAF Receptor in COS-7 Cells—COS-7 cells transfected with the Flag-PAF receptor/pCDM8 plasmid described above were incubated for 20 min at 22 °C with 0 or 3 μM PAF in binding buffer. They were subsequently incubated with 10 μg/ml of anti-Flag M5 monoclonal antibody in Tris-buffered saline containing 1 mM $CaCl_2$ (TBS/Ca), 3% bovine serum albumin, 0.5% normal horse serum, and 0.1% sodium azide for 1 h at 4 °C. Cells were washed 3× with TBS/Ca, fixed with 2% paraformaldehyde in phosphate-buffered saline for 15 min at 4 °C, and incubated with biotinylated horse anti-mouse IgG followed by peroxidase-labeled avidin-biotin complex as recommended by the manufacturers. Cells were stained with 0.05% diaminobenzidine and 0.01% H_2O_2 in TBS/Ca, counterstained with methylene blue, coverslipped with Permount, and photographed.

RESULTS

The guinea pig lung PAF receptor cDNA (13) was prepared by PCR and used to identify an analogous human clone by hybridization with a U937 cell expression library. The longest clone obtained, pCS1, contains a cDNA of approximately 2.8 kb which hybridizes to a single transcript in U937 cell RNA of approximately 4 kb (Fig. 1, *lane A*). Differentiation of the cells with 1 mM dibutyryl-cAMP for 72 h leads to an apparent decrease in abundance of this message (*lane B*). The same ~4-kb transcript is observed in human lung, as shown in *lane C*.

Analysis of genomic DNA with pCS1 under conditions of high stringency reveals a single restriction fragment hybridizing with the probe. As depicted in Fig. 2, digests using *Bam*HI, *Eco*RV, *Hin*dIII, or *Pst*I yield prominent hybridization signals. Analysis of murine genomic DNA digested with the same restriction enzymes, and hybridized and washed under conditions of high stringency reveals a similar pattern, although the fragments are not always the same size (data not shown). These data suggest that pCS1 encodes a single copy gene common to mouse and man. Prolonged exposure of Southern blots reveals a faint background of cross-hybridizing bands, which may reflect related genes (data not shown).

The cDNA and deduced protein sequences of clone CS1 are presented in Fig. 3. The longest open reading frame encodes a protein of 342 amino acids, and search of the EMBL and GenBank data base releases through 1990 revealed no closely related structures. Examination of the deduced protein sequence reveals seven hydrophobic regions interspersed with polar peptide segments characteristic of rhodopsin type G protein-dependent receptors. In contrast to all other identified members of the rhodopsin family of receptors reported to date, including the PAF receptor from guinea pig, the amino-terminal domain of the human PAF receptor does not contain an *N*-linked glycosylation site. An Asn-*X*-Thr/Ser sequence is observed at positions 169–171, and a second potential *N*-linked glycosylation site is found at positions 333–335 at the COOH terminus.

Clone pCS1 in the expression vector pCDM8 was trans-

FIG. 1. Northern analyses of myeloid cell and lung RNA. Two μg of polyadenylated RNA was analyzed under denaturing conditions as described under "Experimental Procedures." *Lane A*, undifferentiated U937 cells; *lane B*, U937 cells differentiated for 72 h with 1 mM dibutyryl-cAMP; *lane C*, human lung parenchyma. A single transcript of ~4 kb was observed to hybridize with cDNA clone pCS1 under conditions of high stringency.

FIG. 2. **Southern analysis of human genomic DNA.** Samples of human genomic DNA (7.5 μg) were electrophoresed following restriction enzyme digestion with *Bam*HI (*lane A*), *Eco*RV (*lane B*), *Hin*dIII (*lane C*), or *Pst*I (*lane D*). Hybridization with radiolabeled cDNA (clone pCS1) at 42 °C with 50% formamide was followed by washing with high stringency buffer (0.2 × SSC, 24 °C, 30 min). Autoradiographs were exposed 18–24 h at −70 °C. The numerals in the *left column* mark the positions of standards (in kb): 12 (12.216), 10 (10.180), 9 (9.162), 7 (7.126), 6 (6.108), 5 (5.090).

fected into COS-7 cells, and the cultures examined for evidence of specific binding of ^{3}H-labeled PAF. This cDNA confers specific binding to COS-7 cells which is not evident in nontransfected cells or in cells transfected with a different cDNA. The rate of uptake of 2 nM ^{3}H-labeled PAF as a function of time at 4 °C is shown in Fig. 4. Under the conditions used, binding approaches equilibrium within 30–40 min. When excess unlabeled PAF is added after 20 min of incubation, approximately 50% of the radiolabeled ligand is displaced following an additional 25 min. As shown in Fig. 5*A*, binding is saturable, and Scatchard analysis of the data indicates a single class of binding sites with an apparent K_d of 5.3 nM (Table I). Specific binding of ^{3}H-labeled PAF to transfected COS-7 cells is blocked by the PAF receptor antagonist, WEB2086, with an ED_{50} of ~5×10^{-6} M (Fig. 5*B*), further supporting the conclusion that clone CS1 encodes a human PAF receptor. When saturation of binding experiments are performed at 4 °C instead of 22 °C, the calculated K_d is essentially identical (5.6 *versus* 5.3 nM) but the apparent number of sites per cell is 8- to 10-fold lower (Table I).

Previous studies of the biological activities of PAF have shown this receptor to be very strongly desensitized to subsequent re-stimulation by ligand (22). In order to determine whether this phenomonon is an intrinsic property of the receptor, PAF receptor-transfected COS-7 cells were preincubated for 20 min at 4 °C with increasing concentrations of PAF, washed, and subsequently incubated with 2 nM ^{3}H-labeled PAF. As shown by the data in Fig. 6, cells preincubated with as little as 1 nM PAF bind only ~30% as much ligand as untreated cells. At this concentration, however, the data presented in Fig. 5*A* indicate that only ~10% of the available receptor sites are bound.

We constructed a Flag-PAF receptor cDNA plasmid, in which the initiating methionine of the natural PAF receptor is mutated to a leucine by PCR and ligated to pCDM8 containing a 5′ adapter encoding the Flag sequence, MDYK-DDDDKEF. The Flag sequence, including the NH_2-terminal methionine residue, is specifically recognized by a monoclonal

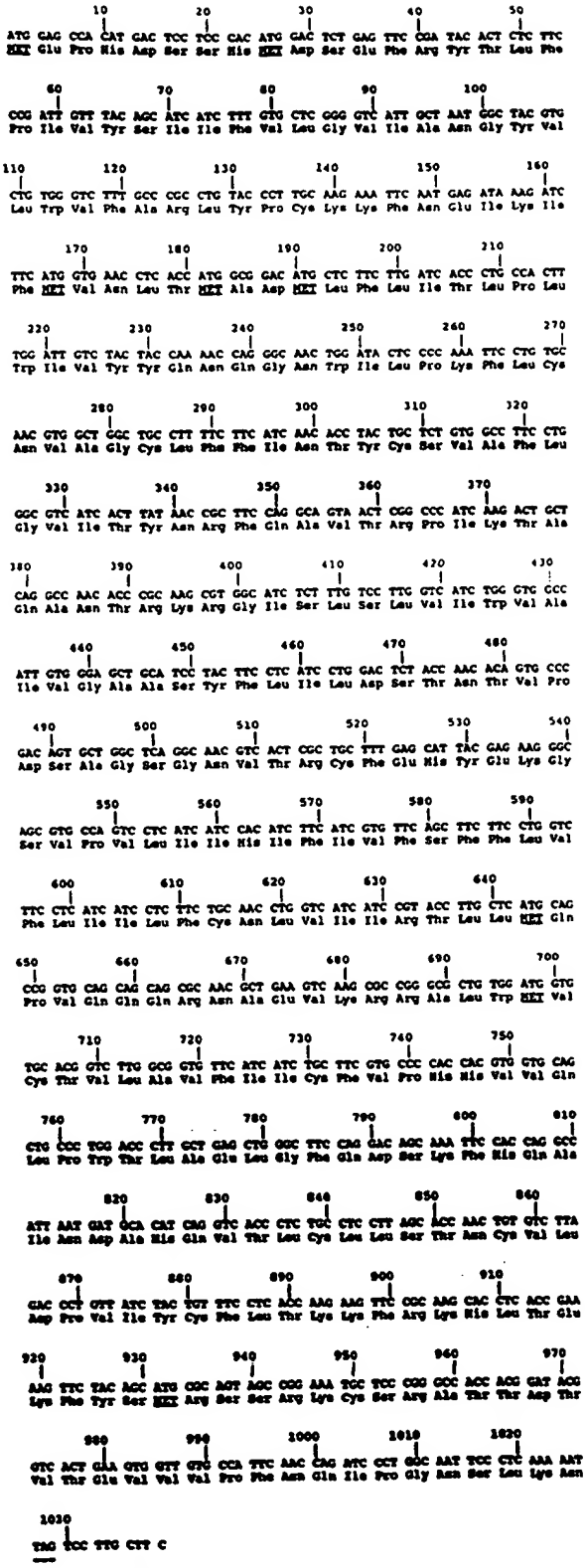


FIG. 3. **cDNA and deduced protein sequence for the human PAF receptor.** Clone pCS1 was sequenced extensively on both strands, and clones from the U937 and HL60 cDNA libraries were identical. The complete coding sequence is depicted, and the deduced protein structure contains 342 amino acids. Primers encompassing the first and last 18 nucleotides depicted are useful in PCR, yielding full length human PAF receptor cDNA.

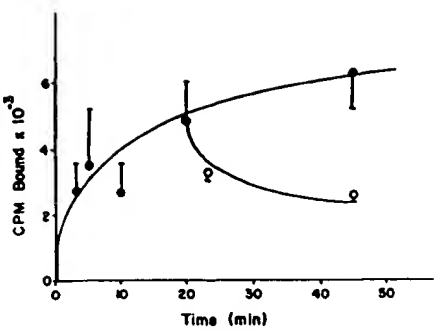


FIG. 4. Kinetics of binding of ^{3}H-labeled PAF to transfected COS-7 cells. COS-7 cells 72 h after transfection with clone pCS1 were incubated with 2 nM ^{3}H-labeled PAF at 4 °C as detailed under "Experimental Procedures." Each point represents the mean of duplicate determinations. Nonspecific binding was assessed by binding in the presence of 10 μM PAF.

antibody, M5, in the presence of millimolar concentrations of calcium (20). Transfection of the Flag-PAF receptor/pCDM8 construct into COS-7 cells also confers specific PAF receptor activity (Fig. 5*A*). Scatchard analysis suggests a slightly lower binding affinity for the ligand, but a similar number of sites per cell (Table I). Thus expression of the Flag-PAF receptor molecule is comparable to the unmodified receptor when transfected into COS cells, and is presumably oriented in a similar manner on the cell membrane. In order to confirm the model for this receptor protein, as illustrated in Fig. 7 which is based on the structure of rhodopsin, transfected cells were stained with the M5 monoclonal antibody followed by secondary antibody and horseradish peroxidase-labeled avidin-biotin complex. As indicated in Fig. 8, the epitope appears to be localized on the extracellular side of the membrane. Nontransfected cells show no staining with this antibody.

DISCUSSION

The U937 cell line is a human lymphoma clone with myeloid characteristics (23), and contains receptors for many proinflammatory mediators including C5a anaphylatoxin, the bacterial chemotaxin, formyl-Met-Leu-Phe, leukotrienes B_4 and D_4, and interleukin-8, as well as PAF (16). Expression of many of these receptors may be modulated positively or negatively by driving differentiation of the cells towards macrophage-like cells with phorbol esters, or towards cells with the phenotype of monocytes and neutrophils with dibutyryl-cAMP (24). The human PAF receptor cDNA was cloned from an undifferentiated U937 cell library by hybridization with the cDNA corresponding to the guinea pig PAF receptor (13). As indicated by the data shown in Fig. 1, differentiation of the cells towards monocytes or neutrophils appears to diminish the abundance of this mRNA. In contrast, expression of the C5a receptor is increased by treatment with dibutyryl-cAMP (16).

Northern blots generated using RNAs from a number of guinea pig tissues, including lung, indicate that the guinea pig PAF receptor cDNA hybridizes with mRNAs of 2.2, 3.0, and 4.0 kb (13). Northern blots of human lung RNA, in contrast, show only a single hybridizing transcript at 4 kb, the same size as obtained with U937 cells (Fig. 1). Size fractionation of the guinea pig RNAs by sucrose density gradient centrifugation followed by expression in *Xenopus* oocytes indicated that the 3.0-kb transcript encodes a functional PAF receptor (13). The human PAF receptor mRNA, however, appears closest in size to the largest of the guinea pig transcripts. It is possible that the lack of expression of the 2.2- and 4.0-kb transcripts in the oocyte relates to mRNA stability or structure, or that the PAF receptor mRNA processing is different in guinea pigs and humans.

Southern blot analysis (Fig. 2) indicates that the human PAF receptor gene exists in a single copy. A similar result

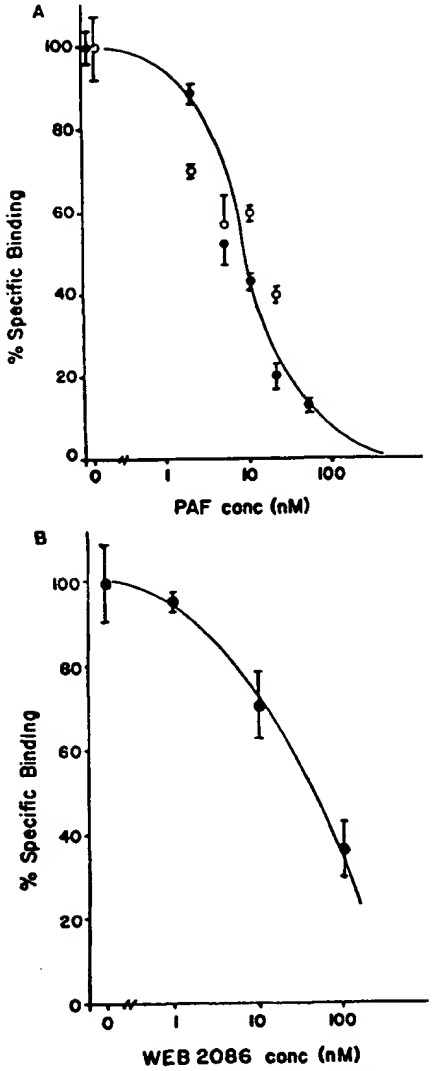


FIG. 5. *A*, binding of ^{3}H-labeled PAF to transfected COS-7 cells. pCS1-transfected COS-7 cells (*closed circles*) or Flag-PAF receptor/pCDM8-transfected cells (*open circles*) were incubated with 2 nM ^{3}H-labeled PAF and increasing concentrations of unlabeled PAF as described under "Experimental Procedures." The apparent K_d values by Scatchard analyses are presented in Table I. *B*, binding was competed effectively by the PAF receptor antagonist WEB2086. Each point represents the mean of duplicate determinations. Nonspecific binding was determined in the presence of 10 μM PAF.

TABLE I

Binding parameters of the human PAF and Flag-PAF receptors transfected in COS-7 cells

Values for K_d and B_{max} were determined from Scatchard analyses of displacement of binding data for each of the constructs transfected into COS-7 cells as described under "Experimental Procedures."

	Temperature	K_d	B_{max}
	°C	nM	fmol/dish
PAF	4	5.6	387
	22	5.3	2350
Flag-PAF	22	13.5	2654

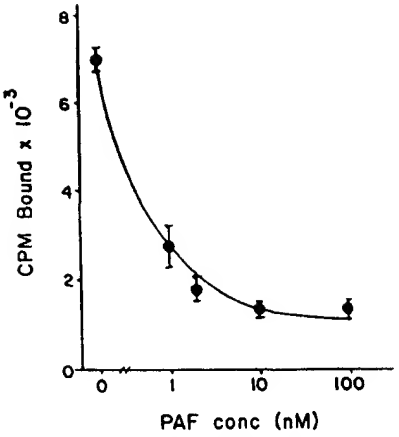


FIG. 6. **PAF receptor desensitization.** Clone pCS1-transfected COS-7 cells were preincubated for 20 min at 4 °C with increasing concentrations of PAF, washed, and incubated with 2 nM ^{3}H-labeled PAF as described under "Experimental Procedures." Each point represents the mean of duplicate determinations. Nonspecific binding was assessed in the presence of 10 μM PAF and these values were subtracted from total binding to obtain the points shown.

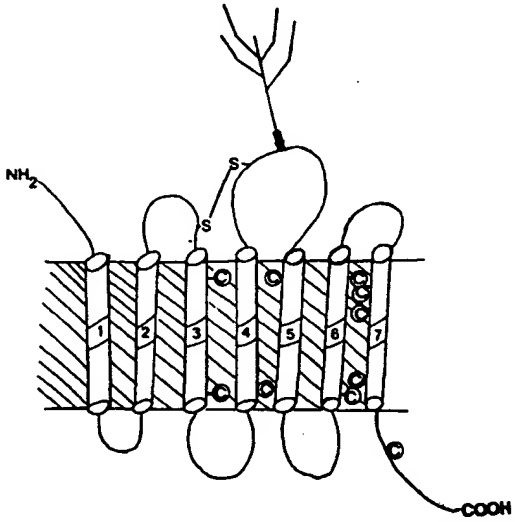


FIG. 7. **Model of the PAF receptor.** The rhodopsin gene family model proposes an exterior amino-terminal region, seven membrane-spanning helices, and a cytoplasmic carboxyl terminus. Special features of the PAF receptor highlighted in the Figure are 9 cysteinyl (C) residues found in the hydrophobic helices, absence of a canonical amino-terminal glycosylation site, and presence of a conserved glycosylation site in the extracellular loop between segments M4 and M5.

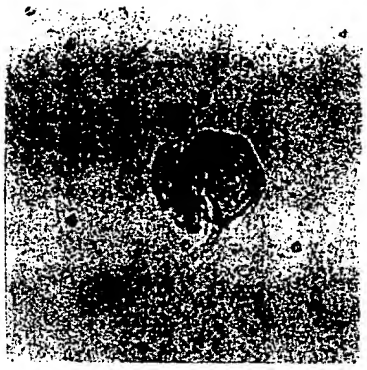


FIG. 8. **Immunohistochemical staining of the human PAF receptor transfected in COS-7 cells.** COS-7 cells transfected with the Flag-PAF receptor/pCDM8 construct were stained with M5 anti-Flag monoclonal antibody, followed by biotinylated anti-mouse and avidin-biotin horseradish peroxidase, as described under "Experimental Procedures." Antibody staining of the PAF receptor is localized to the perimeter of the cell (indicated by *arrows*), characteristic of a cell surface epitope.

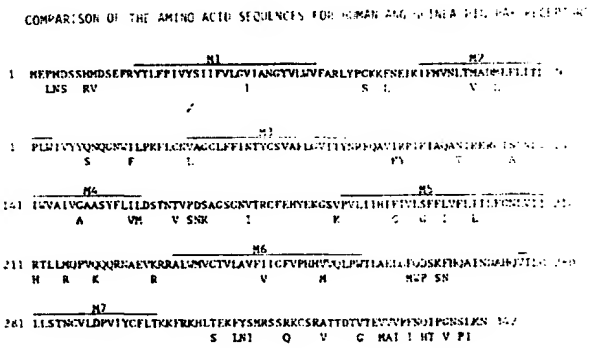


FIG. 9. **Comparison of human and guinea pig PAF receptor protein sequences.** The 342-amino acid human sequence is shown, with the nonidentical residues found in the guinea pig indicated. The seven predicted membrane-spanning domains are indicated by *bars* over the sequence.

was obtained with Southern blots of mouse DNA, although some of the restriction fragments were different sizes. In the guinea pig, it is also possible that the multiple mRNAs observed on Northern blots reflect multiple genes for the PAF receptor in this species. As indicated previously, prolonged exposure of Southern blots of human DNA reveals multiple weakly hybridizing bands. The multiplicity of these bands and the weakness of hybridization suggest that these are related genes as opposed to additional PAF receptor genes. If multiple PAF receptors exist in humans, they may derive from alternative splicing of the mRNA.

Analysis of the deduced amino acid sequence of the human PAF receptor, as noted previously, indicates seven hydrophobic sequences alternating with more polar regions, characteristic of the seven membrane spanning protein members of the rhodopsin family (Fig. 7) (25). The human sequence is ~83% identical to the guinea pig at the amino acid level (Fig. 9). The highest frequency of differences occurs in the COOH-terminal cytoplasmic tail with 18 residues differing among 45. A similar pattern is observed for the receptors for substance P and neurokinin A (26, 27), suggesting less genetic pressure to maintain particular amino acid sequences in this region for effective ligand binding and signal transduction.

Unique to the human PAF receptor among this class of molecules is the absence of an *N*-linked glycosylation site in the NH_2-terminal putative extracellular sequence (25). As noted previously, an *N*-linked glycosylation site occurs at positions 169–171, as it does in the guinea pig, in the putative third extracellular loop. A second glycosylation site exists at positions 333–335, in the COOH-terminal cytoplasmic tail, although this position may not be glycosylated because of its presumed intracellular location. The presence of 12 cysteine residues is also unusual for G-protein coupled receptors. Two of these residues are found in conserved positions in the first and second extracellular loops. By analogy with rhodospin (28), a disulfide bond should link residues 90 and 173. Nine of the remaining 10 cysteine residues are found in putative membrane-spanning segments. Ng and Wong (29) have reported that thiol titrants such as para-chloromercuribenzoate and *N*-ethyl maleimide are capable of altering the affinity of

PAF binding to its receptor. Taken together, these data suggest that there may be free thiol groups in the membrane pore created by the seven transmembrane segments and suggest a potential approach to mapping the PAF-binding site.

Another novel feature in the predicted primary structure of the human PAF receptor is the replacement of a highly conserved asparagine residue in the seventh membrane-spanning segment by aspartic acid. In nearly all G-protein-coupled rhodopsin family receptors reported to date, this asparagine residue is part of a ubiquitous region with the sequence NPXXY; indeed, we have previously exploited this homology to clone the human C5a receptor cDNA (16). Interestingly, the only other reported sequence containing an aspartic acid instead of an asparagine at this position occurs in the thromboxane A_2 receptor (30). As these are the only two lipid receptors of this family whose sequences are known to date, we aligned the thromboxane A_2 and PAF sequences and observed that while the protein sequences are only 19% identical, the nucleotide sequences are 50% identical. Therefore, it is conceivable that these sequences may define a new subclass of the rhodopsin family, and may be useful in low stringency screening to identify receptors for other lipid mediators, including the leukotrienes and prostaglandins.

The ligand-binding properties of the human PAF receptor, expressed in COS-7 cells, are similar to those observed using platelets and neutrophils. The K_d for the human platelet PAF receptor was reported by Hwang *et al.* (5) as 4.9 nM, compared with 5.3 nM for the transfected molecule (Table I), and similar to that reported for the cloned guinea pig receptor also expressed in COS-7 cells (13). Uptake of radiolabeled ligand by the receptor at 4 °C on intact COS cells (Fig. 4) was somewhat slower than that observed previously using platelet membranes (5). This may reflect the use of intact cells in our experiments. The PAF receptor antagonist, WEB2086, blocks ^{3}H-labeled PAF binding, as it does for the guinea pig molecule (13), with an ED_{50} of 5×10^{-8} M.

Additionally, we find 8- to 10-fold higher apparent binding sites per cell when studies are performed at 22 °C instead of at 4 °C (Table I). This may reflect receptor-dependent metabolism of the ligand as described by Homma *et al.* (31), and by Tokumura *et al.* (32). Uptake is exquisitely sensitive to preexposure to PAF, since a 20-min treatment at 4 °C with 1 nM PAF, which results in occupancy of only ~10% of the available receptor sites, blocks subsequent binding of radiolabeled ligand by at least 70%. These findings may reflect internalization of the ligand-receptor complex or some other modification of the receptor (*e.g.* phosphorylation) which renders it unavailable for ligand binding. Indeed, the PAF receptor expressed in COS cells may be a useful system in which to study cellular utilization of PAF as facilitated by its receptor, since no significant uptake occurs on untransfected cells and nonspecific binding is very low.

Because of the utility of the Flag sequence in detection and purification of the C5a anaphylatoxin made in *E. coli* (20), we constructed a Flag-PAF expression plasmid with pCDM8. When transfected into COS-7 cells, the M5 monoclonal antibody, which recognizes the amino acid sequence MDYKDDDDKEF, was used to localize the epitope to the extracellular surface, providing additional support for the rhodopsin-based model for this class of molecules. Previous support of this structure has only been provided by the β-adrenergic receptor, in which a similar approach was utilized (33). This construct should also be useful for studies of ligand-induced changes in receptor localization. Preliminary experiments indicate that PAF pretreatment appears to cause available epitopes to polarize to one end of the cell. Additional experiments using appropriately labeled secondary antibodies or protein A can be used to extend these studies to examine such phenomena as ligand-induced metabolism of the receptor and purification of the receptor protein.

Acknowledgment—We thank Dr. Peter F. Weller, Harvard Medical School, for assistance with the immunohistochemical techniques.

REFERENCES

1. Henson, P. M. (1970) *J. Exp. Med.* **131**, 287-304
2. Snyder, F. (1987) *Platelet-activating Factor and Related Lipid Mediators*, Plenum Publishing Corp., NY
3. Hanahan, D. J. (1986) *Annu. Rev. Biochem.* **55**, 483-509
4. Prescott, S. M., Zimmerman, G. A., and McIntyre, T. M. (1990) *J. Biol. Chem.* **265**, 17381-17384
5. Hwang, S-B., Lee, C-S. C., Cheah, M. J., and Shen, T. Y. (1983) *Biochemistry* **22**, 4756-4763
6. Lad, P. M., Olson, C. V., and Grewal, I. S. (1985) *Biochem. Biophys. Res. Commun.* **129**, 632-638
7. Hwang, S-B., Lam, M-H., and Pong, S-S. (1986) *J. Biol. Chem.* **261**, 532-537
8. Hwang, S-B. (1988) *J. Biol. Chem.* **263**, 3225-3233
9. Paulson, S. K., Wolf, J. L., Novotney-Barry, A., and Cox, C. P. (1990) *Proc. Soc. Exp. Biol. Med.* **195**, 247-254
10. Pinkard, R. N., Farr, R. S., and Hanahan, D. J. (1979) *J. Immunol.* **123**, 1847-1857
11. Blank, M. L., Snyder, F., Byers, L. W., Brooks, B., and Muirhead, E. E. (1979) *Biochem. Biophys. Res. Commun.* **90**, 1194-2000
12. Benveniste, J., Tence, M., Varenne, P., Bidault, J., Boulet, C., and Polonsky, J. (1979) *C. R. Acad. Sci. Ser. D* **289**, 1057-1060
13. Honda, Z-I., Nakamura, M., Miki, I., Minami, M., Watanabe, T., Seyama, Y., Okado, H., Toh, H., Ito, K., Miyamoto, T., and Shimizu, T. (1991) *Nature* **349**, 342-346
14. Chirgwin, J. M., Przybyla, A. E., MacDonald, R. J., and Rutter, W. J. (1979) *Biochemistry* **18**, 5294-5299
15. Gubler, U., and Hoffman, B. (1983) *Gene (Amst.)* **25**, 263-269
16. Gerard, N. P., and Gerard, C. (1991) *Nature* **349**, 614-617
17. Sanger, F., Nicklen, S., and Coulson, A. R. (1977) *Proc. Natl. Acad. Sci. U. S. A.* **74**, 5463-5467
18. Baas, F., Bikker, H., vanOmmen, G-J. B., and deVijlder, J. J. M. (1984) *Hum. Genet.* **67**, 301
19. Aviv, H., and Leder, D. (1972) *Proc. Natl. Acad. Sci. U. S. A.* **69**, 1408-1412
20. Gerard, N. P., and Gerard, C. (1990) *Biochemistry* **29**, 9274-9281
21. Gerard, N. P., Eddy, R. L., Jr., Shows, T. B., and Gerard, C. (1990) *J. Biol. Chem.* **265**, 20455-20462
22. Stimler, N. P., Bloor, C. M., Hugli, T. E., Wykle, R. L., McCall, C. E., and O'Flaherty, J. T. (1981) *Am. J. Pathol.* **105**, 64-69
23. Sundstrom, C., and Nilsson, K. (1976) *Int. J. Cancer* **17**, 565-577
24. Harris, P., and Ralph, P. (1985) *J. Leukocyte Biol.* **37**, 407-422
25. Dohlman, H. G., Thorner, J., Caron, M. G., and Lefkowitz, R. J. (1991) *Annu. Rev. Biochem.* **60**, 653-688
26. Gerard, N. P., Eddy, R. L., Jr., Shows, T. B., and Gerard, C. (1990) *J. Biol. Chem.* **265**, 20455-20462
27. Gerard, N. P., Garraway, L. A., Eddy, R. L., Shows, T. B., Iijima, H., Paquet, J-L., and Gerard, C. (1991) *Biochemistry*, **30**, 10640-10646
28. Karnik, S. S., Sakmar, T. P., Chen, H-B., and Khorana, H. G. (1988) *Proc. Natl. Acad. Sci. U. S. A.* **85**, 8459-8463
29. Ng, D. S., and Wong, K. (1988) *Eur. J. Pharmacol.* **154**, 47-52
30. Hirata, M., Hayashi, Y., Ushikubi, F., Yokota, Y., Kageyama, R., Nakanishi, S., and Narumiyai, S. (1991) *Nature* **349**, 617-620
31. Homma, H., Tokumura, A., and Hanahan, D. J. (1987) *J. Biol. Chem.* **262**, 10582-10587
32. Tokumura, A., Tutsumi, T., Yoshida, J., and Tsukatani, H. (1990) *Biochim. Biophys. Acta* **1044**, 91-100
33. Wang, H., Lipfert, L., Malbon, C. C., and Bahouth, S. (1989) *J. Biol. Chem.* **264**, 14424-14431
34. Nakamura, M., Hondo, Z.-I., Izumi, T., Sakanaka, C., Mutoh, H., Minami, M., Bito, H., Seyama, Y., Matsumoto, T., Noma, M., and Shimizu, T. (1991) *J. Biol. Chem.* **266**, 20400-20405
35. Ye, R. D., Prossnitz, E. R., Zou, A. M., and Cochrane, C. G. (1991) *Biochem. Biophys. Res. Commun.* **180**, 105-111

NCBI results of BLAST

BLASTN 2.2.8 [Jan-05-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079535895-1755-55097089079.BLASTQ3

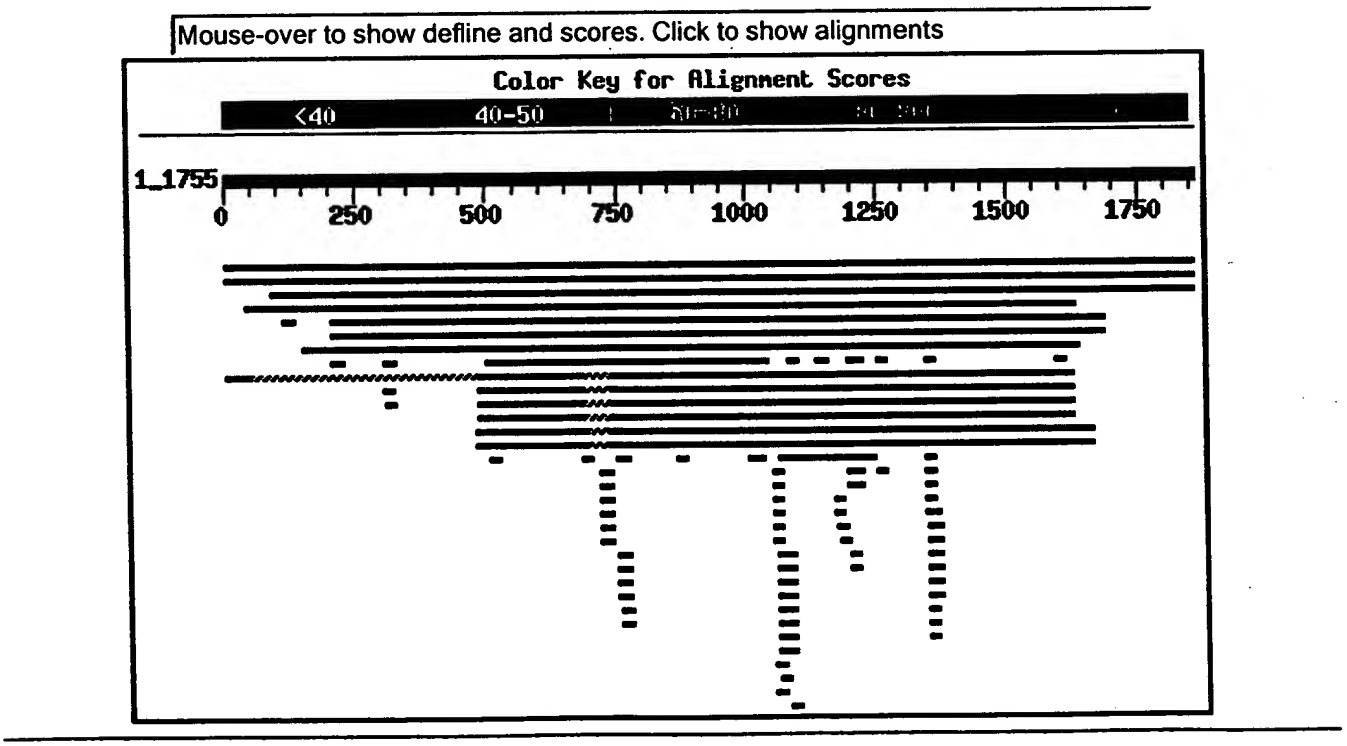
Query=
(1860 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
2,102,977 sequences; 10,130,642,339 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 91 Blast Hits on the Query Sequence



Sequences producing significant alignments:	Score (bits)	E Value	
gi|13159911|emb|AL159140.4|CNS01RGP Human chromosome 14 DNA...	3663	0.0	
gi|15282112|emb|AL162471.3|CNS01RHU Human chromosome 14 DNA...	3640	0.0	
gi|34190130|gb|BC032831.2| Homo sapiens cDNA clone MGC:2673...	3489	0.0	L U
gi|21928412|dbj|AB065563.1| Homo sapiens gene for seven tra...	3128	0.0	L
gi|32165519|gb|AY288418.1| Homo sapiens G protein-coupled r...	2920	0.0	L U
gi|32261308|ref|NM_022571.3| Homo sapiens G protein-coupled...	2920	0.0	L U G
gi|2810988|gb|M76676.1|HUMNPIIY20 Homo sapiens leukocyte pl...	2700	0.0	L U G
gi|29611577|gb|AY255588.1| Homo sapiens leukocyte platelet-...	1082	0.0	L U
gi|38565931|gb|BC062104.1| Mus musculus cDNA clone IMAGE:68...	803	0.0	L
gi|32165533|gb|AY288425.1| Mus musculus G protein-coupled r...	803	0.0	L U
gi|32964966|gb|AC110170.6| Mus musculus chromosome 12, clon...	803	0.0	
gi|32306523|ref|NM_181752.1| Mus musculus G protein-coupled...	803	0.0	L U
gi|32165543|gb|AY288430.1| Rattus norvegicus G protein-coup...	783	0.0	L U
gi|32401462|ref|NM_181771.1| Rattus norvegicus G protein-co...	783	0.0	L U
gi|32563165|emb|BX004994.6| Zebrafish DNA sequence from clo...	137	9e-29	
gi|6031165|ref|NM_001480.2| Homo sapiens galanin receptor 1...	46	0.25	L U G
gi|24648696|ref|NM_169955.1| Drosophila melanogaster CG1082...	46	0.25	L U
gi|24648694|ref|NM_142709.1| Drosophila melanogaster CG1082...	46	0.25	L U
gi|34895453|ref|NM_184181.1| Oryza sativa (japonica cultiva...	46	0.25	U
gi|33589379|gb|BT009988.1| Drosophila melanogaster RE47636 ...	46	0.25	
gi|14090356|dbj|AP003233.3| Oryza sativa (japonica cultivar...	46	0.25	
gi|21629409|gb|AC100863.2| Homo sapiens chromosome 18, clon...	46	0.25	
gi|23171864|gb|AE003734.2| Drosophila melanogaster chromoso...	46	0.25	L
gi|25140120|gb|AC096709.19| Homo sapiens chromosome 18, clo...	46	0.25	
gi|17861010|gb|AC008308.8| Drosophila melanogaster, chromos...	46	0.25	
gi|16258972|gb|AC008309.7| Drosophila melanogaster, chromos...	46	0.25	
gi|44355566|gb|AY541036.1| Homo sapiens galanin receptor 1 ...	46	0.25	
gi|3064071|gb|U90658.1|HSGALNRS1 Homo sapiens galanin recep...	46	0.25	L
gi|1297337|gb|U53511.1|HSU53511 Homo sapiens galanin recept...	46	0.25	L U
gi|775209|gb|U23854.1|HSU23854 Human galanin receptor mRNA,...	46	0.25	L U
gi|559047|gb|L34339.1|HUMGALAREC Human galanin receptor mRN...	46	0.25	L U
gi|12328514|dbj|AP002909.2| Oryza sativa (japonica cultivar...	46	0.25	
gi|22296778|gb|AC121870.2| Mus musculus BAC clone RP24-121D...	44	0.98	
gi|13677146|gb|AC013726.7| Homo sapiens BAC clone RP11-400N...	44	0.98	
gi|29609103|dbj|AP005043.1| Streptomyces avermitilis genomi...	44	0.98	
gi|5001541|gb|AC005520.2|AC005520 Homo sapiens PAC clone RP...	44	0.98	
gi|21212029|emb|AL662811.20| Mouse DNA sequence from clone ...	44	0.98	
gi|33457241|gb|AC127554.4| Mus musculus BAC clone RP24-323K...	42	3.9	
gi|21618432|gb|BC032702.1| Homo sapiens G protein-coupled r...	42	3.9	L U G
gi|28630143|gb|AC124170.3| Mus musculus BAC clone RP23-155H...	42	3.9	
gi|38089509|ref|XM_357908.1| Mus musculus similar to SON pr...	42	3.9	L U
gi|37533899|ref|NM_196270.1| Oryza sativa (japonica cultiva...	42	3.9	U
gi|23325376|gb|AE014636.1| Bifidobacterium longum NCC2705 s...	42	3.9	
gi|32567975|gb|AC105258.2| Oryza sativa (japonica cultivar-...	42	3.9	
gi|31431814|gb|AE017089.1| Oryza sativa (japonica cultivar-...	42	3.9	
gi|24418066|gb|AC009108.10| Homo sapiens chromosome 16 clon...	42	3.9	
gi|44886087|dbj|AB164051.1| Oryzias latipes cGK I beta mRNA...	42	3.9	
gi|44886085|dbj|AB164050.1| Oryzias latipes cGK I alpha mRN...	42	3.9	
gi|29366932|gb|AC009033.10| Homo sapiens chromosome 16 clon...	42	3.9	

gi|13424739|gb|AE005972.1| Caulobacter crescentus CB15 sect...	42	3.9	
gi|21108849|gb|AE011898.1| Xanthomonas axonopodis pv. citri...	42	3.9	
gi|21108642|gb|AE011876.1| Xanthomonas axonopodis pv. citri...	42	3.9	
gi|21115400|gb|AE012537.1| Xanthomonas campestris pv. campe...	42	3.9	
gi|21741993|emb|AL662970.2|OSJN00174 Oryza sativa genomic D...	42	3.9	
gi|32975800|dbj|AK065782.1| Oryza sativa (japonica cultivar...	42	3.9	U
gi|18057076|gb|AC024591.4| Homo sapiens chromosome 16 clone...	42	3.9	
gi|29609643|dbj|AP005045.1| Streptomyces avermitilis genomi...	42	3.9	
gi|455487|dbj|D21062.1|MUSGPCR21 Mus musculus GPCR21 mRNA f...	42	3.9	L U G
gi|22531332|emb|AJ420781.1|XLA420781 Xenopus laevis mRNA fo...	42	3.9	L U
gi|1545939|emb|X94402.1|FRCB1B F.rubripes CB1B gene for can...	42	3.9	
gi|1890580|emb|Z79692.1|RMEXPGNS R.meliloti exp gene cluster	42	3.9	
gi|15140691|emb|AL603645.1|RME603645 Rhizobium meliloti (Si...	42	3.9	
gi|24418991|emb|AL939105.1|SCO939105 Streptomyces coelicolo...	42	3.9	
gi|5679837|emb|AJ243961.1|OSA243961 Oryza sativa chromosome...	42	3.9	
gi|6634702|emb|AJ131718.1|ZMA131718 Zea mays mRNA for legum...	42	3.9	U
gi|17430467|emb|AL646076.1| Ralstonia solanacearum GMI1000 ...	42	3.9	
gi|1834557|emb|Z84846.1|HSZ84846 H.sapiens gene encoding im...	42	3.9	
gi|1834538|emb|Z84827.1|HSZ84827 H.sapiens gene encoding im...	42	3.9	
gi|13625390|gb|AF346834.1|AF346834 Mus musculus forkhead pr...	42	3.9	L
gi|4902626|emb|AL033397.7|HS27K12 Human DNA sequence from c...	42	3.9	
gi|10444099|gb|AF283762.1|AF283762 Mus musculus mouse-thyro...	42	3.9	L U G
gi|10140611|gb|AC078839.4|AC078839 Genomic Sequence For Ory...	42	3.9	
gi|12706033|gb|AY022817.1| Oryza sativa microsatellite MRG5...	42	3.9	
gi|632504|gb|U18550.1|HSU18550 Human GPR3 G protein-coupled...	42	3.9	L G
gi|16605732|emb|AL591003.16| Mouse DNA sequence from clone ...	42	3.9	
gi|10334464|emb|AL355296.12| Human DNA sequence from clone ...	42	3.9	
gi|6680064|ref|NM_008154.1| Mus musculus G-protein coupled ...	42	3.9	L U G
gi|6465842|emb|AL096774.9|HSDJ144C9 Human DNA sequence from...	42	3.9	L
gi|1061125|emb|X83956.1|HSACCAGEN H.sapiens ACCA gene	42	3.9	L
gi|8218068|emb|AL078590.28|HSA557H15 Human DNA sequence fro...	42	3.9	
gi|602311|gb|L32831.1|HUMGPCRD Homo sapiens G protein-coupl...	42	3.9	L G
gi|31377791|ref|NM_005281.2| Homo sapiens G protein-coupled...	42	3.9	L U G
gi|21738486|emb|AL671858.6| Mouse DNA sequence from clone R...	42	3.9	
gi|18875347|ref|NM_133202.1| Mus musculus thyrotropin relea...	42	3.9	L U

Alignments

>gi|13159911|emb|AL159140.4|CNS01RGP D Human chromosome 14 DNA sequence BAC R-131E chromosome 14 of Homo sapiens (Human), complete sequence

Length = 164452

Score = 3663 bits (1848), Expect = 0.0
Identities = 1775/1860 (95%)
Strand = Plus / Minus

```
Query: 1      cgctcctgcgtaaacacgcggttccctcggcaacgctggaacccacgtcaaaggctccgc 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129187 cgctcctgcgtaaacacgcggttccctcggcaacgctggaacccacgtcaaaggctccgc 129128

Query: 61     caggtccccagcgaccgccacccctccggccgagcccagctccccgcggcggccgctagc 120
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129127 caggtccccagcgaccgccacccctccggccgagcccagctccccgcggcggccgctagc 129068

Query: 121    ccccggccccgagccaccactccgacctagcggccgccgcccccggtgcgggatgaggag 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129067 ccccggccccgagccaccactccgacctagcggccgccgcccccggtgcgggatgaggag 129008

Query: 181    atccgcggccgccactgggccccatggaggagccgcagccgccccgcccaccagcgagca 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 129007 atccgcggccgccactgggccccatggaggagccgcagccgccccgcccaccagcgagca 128948

Query: 241    tggccttactgggcagccagcactccggcgccccctccgcggccggcccacctggcggga 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128947 tggccttactgggcagccagcactccggcgccccctccgcggccggcccacctggcggga 128888

Query: 301    cttcctccgcggccacggcggccgtgctctccttcagcaccgtggcgaccgcggcgctgg 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128887 cttcctccgcggccacggcggccgtgctctccttcagcaccgtggcgaccgcggcgctgg 128828

Query: 361    ggaacctgagcgacgcaagcggaggcggcacagctgccgcnnnnnnnnnnnnnnnnnnn 420
               ||||||||||||||||||||||||||||||||||||||||
Sbjct: 128827 ggaacctgagcgacgcaagcggaggcggcacagctgccgctcccggtggcggcggccttg 128768

Query: 421    nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 480

Sbjct: 128767 gcgggtccggggcagcgcgggaggcgggggcggcggtgaggcggccgctaggcccggagg 128708

Query: 481    nnnnnccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128707 cggcgccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 128648

Query: 541    tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128647 tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 128588

Query: 601    agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128587 agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 128528

Query: 661    cgctgctctgcctgcccgccgccttcctggacctcttcactccgcccgggggttcggcgc 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128527 cgctgctctgcctgcccgccgccttcctggacctcttcactccgcccgggggttcggcgc 128468

Query: 721    ctgccgccgccgcggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgt 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128467 ctgccgccgccgcggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgt 128408

Query: 781    gcttcggcatcgtgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgcta 840
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128407 gcttcggcatcgtgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgcta 128348

Query: 841    tcgtgcggccgccgcgggagaaagatcggccgccgccgcgcgctgcagctgctggcgggcg 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128347 tcgtgcggccgccgcgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcg 128288

Query: 901    cctggctgacggccctgggcttctccttgccctgggagctgctcggggcgccccgggaac 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128287 cctggctgacggccctgggcttctccttgccctgggagctgctcggggcgccccgggaac 128228

Query: 961    tcgcggcggcgcagagcttccacggctgcctctaccggacctccccggaccccgcgcagc 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128227 tcgcggcggcgcagagcttccacggctgcctctaccggacctccccggaccccgcgcagc 128168

Query: 1021   tgggcgcggccttcagcgtggggctggtggtggcctgctacctgctgcccttcctgctca 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128167 tgggcgcggccttcagcgtggggctggtggtggcctgctacctgctgcccttcctgctca 128108

Query: 1081   tgtgcttctgccactaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggc 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128107 tgtgcttctgccactaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggc 128048

Query: 1141   cggtgaacacctacgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccg 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 128047 cggtgaacacctacgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccg 127988

Query: 1201   tcctcatcatgatcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgc 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127987 tcctcatcatgatcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgc 127928

Query: 1261   tggccgccgcccggcaggcccagaccatgcaggccccctcgctcctcagcgtggtggccg 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127927 tggccgccgcccggcaggcccagaccatgcaggccccctcgctcctcagcgtggtggccg 127868

Query: 1321   tctggctgacctgggccaatggggccatcaaccctgtcatctacgccatccgcaatccca 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127867 tctggctgacctgggccaatggggccatcaaccctgtcatctacgccatccgcaatccca 127808

Query: 1381   acatttcgatgctcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacg 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127807 acatttcgatgctcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacg 127748

Query: 1441   ctttcctgcccagccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaacc 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127747 ctttcctgcccagccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaacc 127688

Query: 1501   gctatgccaaccggctgggggcctgcaacaggatgtcctcttccaacccggccagcggag 1560
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127687 gctatgccaaccggctgggggcctgcaacaggatgtcctcttccaacccggccagcggag 127628


Query: 1561   tggcaggggacgtggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagg 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127627 tggcaggggacgtggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagg 127568


Query: 1621   gaccaccagagccggtgacggcagtgaccaaacagcctaaatccgaagctggggatacca 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127567 gaccaccagagccggtgacggcagtgaccaaacagcctaaatccgaagctggggatacca 127508


Query: 1681   gcctctaagacggttggaatggccagcttatgaaggcaaatttccactcgcattatttaa 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127507 gcctctaagacggttggaatggccagcttatgaaggcaaatttccactcgcattatttaa 127448


Query: 1741   tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127447 tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 127388


Query: 1801   acgggggaggcttaccactttccccaaacaacataaaagacaatgtcccttcttcaaaag 1860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 127387 acgggggaggcttaccactttccccaaacaacataaaagacaatgtcccttcttcaaaag 127328
```

>gi|15282112|emb|AL162471.3|CNS01RHU Human chromosome 14 DNA sequence Partial se
library RPCI-11 from chromosome 14 of Homo sapiens
(Human), complete sequence
Length = 149326

Score = 3640 bits (1836), Expect = 0.0
Identities = 1772/1860 (95%)
Strand = Plus / Plus

```
Query: 1      cgctcctgcgtaaacacgcggttccctcggcaacgctggaacccacgtcaaaggctccgc 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 57931 cgctcctgcgtaaacacgcggttccctcggcaacgctggaacccacgtcaaaggctccgc 57990


Query: 61     caggtccccagcgaccgccacccctccggccgagcccagctccccgcggcggccgctagc 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 57991 caggtccccagcgaccgccacccctccggccgagcccagctccccgcggcggccgctagc 58050


Query: 121    ccccggccccgagccaccactccgacctagcggccgccgcccccggtgcgggatgaggag 180
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct: 58051 ccccggccccgagccaccactccgacctagtggccgccgcccccggtgcgggatgaggag 58110


Query: 181    atccgcggccgccactgggccccatggaggagccgcagccgccccgcccaccagcgagca 240
               ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct: 58111 atccgcggccgccactgggccccatggaggagccgccgccgccccgcccaccagcgagca 58170
```

```
Query: 241   tggccttactgggcagccagcactccggcgccccctccgcggccggcccacctggcggga 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58171 tggccttactgggcagccagcactccggcgccccctccgcggccggcccacctggcggga 58230

Query: 301   cttcctccgcggccacggcggccgtgctctccttcagcaccgtggcgaccgcggcgctgg 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58231 cttcctccgcggccacggcggccgtgctctccttcagcaccgtggcgaccgcggcgctgg 58290

Query: 361   ggaacctgagcgacgcaagcggaggcggcacagctgccgcnnnnnnnnnnnnnnnnnnn 420
             ||||||||||||||||||||||||||||||||||||
Sbjct: 58291 ggaacctgagcgacgcaagcggaggcggcacagctgccgctcccggtggcggcggccttg 58350

Query: 421   nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 480

Sbjct: 58351 gcgggtccggggcagcgcgggaggcgggggcggcggtgaggcggccgctaggcccggagg 58410

Query: 481   nnnnnccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 540
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58411 cggcgccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 58470

Query: 541   tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58471 tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 58530

Query: 601   agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58531 agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 58590

Query: 661   cgctgctctgcctgcccgccgccttcctggacctcttcactccgcccgggggttcggcgc 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58591 cgctgctctgcctgcccgccgccttcctggacctcttcactccgcccgggggttcggcgc 58650

Query: 721   ctgccgccgccgcggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgt 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58651 ctgccgccgccgcggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgt 58710

Query: 781   gcttcggcatcgtgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgcta 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58711 gcttcggcatcgtgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgcta 58770

Query: 841   tcgtgcggccgccgcgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcg 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58771 tcgtgcggccgccgcgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcg 58830

Query: 901   cctggctgacggccctgggcttctccttgccctgggagctgctcggggcgccccgggaac 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58831 cctggctgacggccctgggcttctccttgccctgggagctgctcggggcgccccgggaac 58890
```

```
Query: 961   tcgcggcggcgcagagcttccacggctgcctctaccggacctccccggaccccgcgcagc 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58891 tcgcggcggcgcagagcttccacggctgcctctaccggacctccccggaccccgcgcagc 58950

Query: 1021  tgggcgcggccttcagcgtggggctggtggtggcctgctacctgctgcccttcctgctca 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58951 tgggcgcggccttcagcgtggggctggtggtggcctgctacctgctgcccttcctgctca 59010

Query: 1081  tgtgcttctgccactaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggc 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59011 tgtgcttctgccactaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggc 59070

Query: 1141  cggtgaacacctacgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccg 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59071 cggtgaacacctacgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccg 59130

Query: 1201  tcctcatcatgatcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgc 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59131 tcctcatcatgatcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgc 59190

Query: 1261  tggccgccgcccggcaggcccagaccatgcaggcccctcgctcctcagcgtggtggccg 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59191 tggccgccgcccggcaggcccagaccatgcaggcccctcgctcctcagcgtggtggccg 59250

Query: 1321  tctggctgacctgggccaatggggccatcaaccctgtcatctacgccatccgcaatccca 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59251 tctggctgacctgggccaatggggccatcaaccctgtcatctacgccatccgcaatccca 59310

Query: 1381  acatttcgatgctcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacg 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59311 acatttcgatgctcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacg 59370

Query: 1441  ctttcctgcccagccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaacc 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59371 ctttcctgcccagccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaacc 59430

Query: 1501  gctatgccaaccggctgggggcctgcaacaggatgtcctcttccaacccggccagcggag 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59431 gctatgccaaccggctgggggcctgcaacaggatgtcctcttccaacccggccagcggag 59490

Query: 1561  tggcaggggacgtggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagg 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59491 tggcaggggacgtggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagg 59550

Query: 1621  gaccaccagagccggtgacggcagtgaccaaacagcctaaatccgaagctggggatacca 1680
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct: 59551 gaccaccagagccggtgacggcagcgaccaaacagcctaaatccgaagctggggatacca 59610
```

```
Query: 1681  gcctctaagacggttggaatggccagcttatgaaggcaaatttccactcgcattatttaa 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59611 gcctctaagacggttggaatggccagcttatgaaggcaaatttccactcgcattatttaa 59670

Query: 1741  tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59671 tgatggaagattctgggggagagttgtggatttcataaagccaaacatttaaagctagag 59730

Query: 1801  acgggggaggcttaccactttccccaaacaacataaaagacaatgtcccttcttcaaaag 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 59731 acgggggaggcttaccactttccccaaacaacataaaagacaatgtcccttcttcaaaag 59790
```

>gi|34190130|gb|BC032831.2| LU Homo sapiens cDNA clone MGC:26730 IMAGE:4825908, c
Length = 2557

Score = 3489 bits (1760), Expect = 0.0
Identities = 1687/1772 (95%)
Strand = Plus / Plus

```
Query: 89    gccgagcccagctccccgcggcggccgctagcccccggccccgagccaccactccgacct 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1      gccgagcccagctccccgcggcggccgctagcccccggccccgagccaccactccgacct 60

Query: 149   agcggccgccgcccccggtgcgggatgaggagatccgcggccgccactgggccccatgga 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61     agcggccgccgcccccggtgcgggatgaggagatccgcggccgccactgggccccatgga 120

Query: 209   ggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcactccgg 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   ggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcactccgg 180

Query: 269   cgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggccgtgct 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   cgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggccgtgct 240

Query: 329   ctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcgg 388
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   ctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcgg 300

Query: 389   cacagctgccgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 448
              ||||||||||||
Sbjct: 301   cacagctgccgctcccggtggcggcggccttggcgggtccggggcagcgcgggaggcggg 360

Query: 449   nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacggagctgc 508
                                                   ||||||||||||||||||||||
Sbjct: 361   ggcggcggtgaggcggccgctaggcccggaggcggcgccgctgctgtcgcacggagctgc 420

Query: 509   agtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactg 568
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  agtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactg 480

Query: 569  cgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcat 628
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  cgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcat 540

Query: 629  cctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcct 688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  cctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcct 600

Query: 689  ggacctcttcactccgcccgggggttcggcgcctgccgccgccgcggggccctggcgcgg 748
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  ggacctcttcactccgcccgggggttcggcgcctgccgccgccgcggggccctggcgcgg 660

Query: 749  cttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgt 808
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  cttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgt 720

Query: 809  ggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaagatcgg 868
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  ggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaagatcgg 780

Query: 869  ccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttctcctt 928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttctcctt 840

Query: 929  gccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccacggctg 988
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  gccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccacggctg 900

Query: 989  cctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtggggctggt 1048
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  cctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtggggctggt 960

Query: 1049 ggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaa 1108
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  ggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaa 1020

Query: 1109 gacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcg 1168
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 gacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcg 1080

Query: 1169 cttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctg 1228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081 cttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctg 1140

Query: 1229 ctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccagaccat 1288
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 ctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccagaccat 1200


Query: 1289 gcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccat 1348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 gcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccat 1260


Query: 1349 caaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccg 1408
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 caaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccg 1320


Query: 1409 cgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccgggtct 1468
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 cgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccgggtct 1380


Query: 1469 gcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaa 1528
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 gcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaa 1440


Query: 1529 caggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgggcccg 1588
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 caggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgggcccg 1500


Query: 1589 caaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggcagtgac 1648
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1501 caaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggcagtgac 1560


Query: 1649 caaacagcctaaatccgaagctggggataccagcctctaagacggttggaatggccagct 1708
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1561 caaacagcctaaatccgaagctggggataccagcctctaagacggttggaatggccagct 1620


Query: 1709 tatgaaggcaaatttccactcgcattatttaatgatggaagattctgggggagagttgtg 1768
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1621 tatgaaggcaaatttccactcgcattatttaatgatggaagattctgggggagagttgtg 1680


Query: 1769 gatttcataaagccaaacatttaaagctagagacgggggaggcttaccactttccccaaa 1828
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1681 gatttcataaagccaaacatttaaagctagagacgggggaggcttaccactttccccaaa 1740


Query: 1829 caacataaaagacaatgtcccttcttcaaaag 1860
            ||||||||||||||||||||||||||||||
Sbjct: 1741 caacataaaagacaatgtcccttcttcaaaag 1772
```

>gi|21928412|dbj|AB065563.1| Homo sapiens gene for seven transmembrane helix rec
cds, isolate:CBRC7TM_126
Length = 1590

Score = 3128 bits (1578), Expect = 0.0

```
 Identities = 1505/1590 (94%)
 Strand = Plus / Plus

Query: 40   aacccacgtcaaaggctccgccaggtccccagcgaccgccacccctccggccgagcccag 99
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    aacccacgtcaaaggctccgccaggtccccagcgaccgccacccctccggccgagcccag 60

Query: 100  ctccccgcggcggccgctagcccccggccccgagccaccactccgacctagcggccgccg 159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   ctccccgcggcggccgctagcccccggccccgagccaccactccgacctagcggccgccg 120

Query: 160  cccccggtgcgggatgaggagatccgcggccgccactgggccccatggaggagccgcagc 219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  cccccggtgcgggatgaggagatccgcggccgccactgggccccatggaggagccgcagc 180

Query: 220  cgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgcccccctccg 279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  cgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgcccccctccg 240

Query: 280  cggccggcccacctggcgggacttcctccgcggccacggcggccgtgctctccttcagca 339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  cggccggcccacctggcgggacttcctccgcggccacggcggccgtgctctccttcagca 300

Query: 340  ccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcggcacagctgccg 399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  ccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcggcacagctgccg 360

Query: 400  cnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 459
            |
Sbjct: 361  ctcccggtggcggcggccttggcgggtccggggcagcgcgggaggcgggggcggcggtga 420

Query: 460  nnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacggagctgcagtggcggccc 519
                                      ||||||||||||||||||||||||||||||||||
Sbjct: 421  ggcggccgctaggcccggaggcggcgccgctgctgtcgcacggagctgcagtggcggccc 480

Query: 520  aggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactgcgcggtgatgg 579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  aggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactgcgcggtgatgg 540

Query: 580  gggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcatcctgtcgctgt 639
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  gggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcatcctgtcgctgt 600

Query: 640  ccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcctggacctcttca 699
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  ccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcctggacctcttca 660

Query: 700  ctccgcccgggggttcggcgcctgccgccgccgcggggccctggcgcggcttctgcgccg 759
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  ctccgcccgggggttcggcgcctgccgccgccgcggggccctggcgcggcttctgcgccg 720

Query: 760  ccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgtggcgctcatct 819
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  ccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgtggcgctcatct 780

Query: 820  cgttggaccgttactgcgctatcgtgcggccgccgcgggagaagatcggccgccgccgcg 879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  cgttggaccgttactgcgctatcgtgcggccgccgcgggagaagatcggccgccgccgcg 840

Query: 880  cgctgcagctgctggcgggcgcctggctgacggccctgggcttctccttgccctgggagc 939
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  cgctgcagctgctggcgggcgcctggctgacggccctgggcttctccttgccctgggagc 900

Query: 940  tgctcggggcgccccgggaactcgcggcggcgcagagcttccacggctgcctctaccgga 999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  tgctcggggcgccccgggaactcgcggcggcgcagagcttccacggctgcctctaccgga 960

Query: 1000 cctccccggaccccgcgcagctgggcgcggccttcagcgtggggctggtggtggcctgct 1059
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  cctccccggaccccgcgcagctgggcgcggccttcagcgtggggctggtggtggcctgct 1020

Query: 1060 acctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaagacggtgcgcc 1119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 acctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaagacggtgcgcc 1080

Query: 1120 tgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcgcttcttcagcg 1179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081 tgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcgcttcttcagcg 1140

Query: 1180 aggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgctgctgggggc 1239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 aggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgctgctgggggc 1200

Query: 1240 cctactgcttcctggtgctgctggccgccgcccggcaggcccagaccatgcaggccccct 1299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 cctactgcttcctggtgctgctggccgccgcccggcaggcccagaccatgcaggccccct 1260

Query: 1300 cgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatcaaccctgtca 1359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 cgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatcaaccctgtca 1320

Query: 1360 tctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgcgaggagggct 1419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 tctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgcgaggagggct 1380

Query: 1420 accggactaggaatgtggacgctttcctgcccagccagggcccgggtctgcaagccagaa 1479
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 accggactaggaatgtggacgctttcctgcccagccagggcccgggtctgcaagccagaa 1440


Query: 1480 gccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaacaggatgtcct 1539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 gccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaacaggatgtcct 1500


Query: 1540 cttccaacccggccagcggagtggcaggggacgtggccatgtgggcccgcaaaaatccag 1599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1501 cttccaacccggccagcggagtggcaggggacgtggccatgtgggcccgcaaaaatccag 1560


Query: 1600 ttgtacttttctgccgagagggaccaccag 1629
            ||||||||||||||||||||||||||||||
Sbjct: 1561 ttgtacttttctgccgagagggaccaccag 1590
```

>gi|32165519|gb|AY288418.1| Homo sapiens G protein-coupled receptor 135 (GPR13

cds

Length = 1485

Score = 2920 bits (1473), Expect = 0.0
Identities = 1400/1485 (94%)
Strand = Plus / Plus

```
Query: 204  atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 263
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 60


Query: 264  tccggcgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggcc 323
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   tccggcgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggcc 120


Query: 324  gtgctctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcgga 383
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gtgctctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcgga 180


Query: 384  ggcggcacagctgccgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 443
             ||||||||||||||||
Sbjct: 181  ggcggcacagctgccgctcccggtggcggcggccttggcgggtccggggcagcgcgggag 240


Query: 444  nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacgga 503
                                                      ||||||||||||||||||
Sbjct: 241  gcgggggcggcggtgaggcggccgctaggcccggaggcggcgccgctgctgtcgcacgga 300


Query: 504  gctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggc 563
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  gctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggc 360


Query: 564  aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 623
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 420

Query: 624  ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgcc 683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgcc 480

Query: 684  ttcctggacctcttcactccgcccgggggttcggcgcctgccgccgccgcggggccctgg 743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  ttcctggacctcttcactccgcccgggggttcggcgcctgccgccgccgcggggccctgg 540

Query: 744  cgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  cgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 600

Query: 804  agcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaag 863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  agcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaag 660

Query: 864  atcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttc 923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  atcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttc 720

Query: 924  tccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccac 983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  tccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccac 780

Query: 984  ggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtgggg 1043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtgggg 840

Query: 1044 ctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatc 1103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  ctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatc 900

Query: 1104 tgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 1163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  tgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 960

Query: 1164 ctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  ctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1020

Query: 1224 atctgctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccag 1283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 atctgctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccag 1080

Query: 1284 accatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggg 1343
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081 accatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggg 1140


Query: 1344 gccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgc 1403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 gccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgc 1200


Query: 1404 aaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccg 1463
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 aaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccg 1260


Query: 1464 ggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcc 1523
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 ggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcc 1320


Query: 1524 tgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgg 1583
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 tgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgg 1380


Query: 1584 gcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggca 1643
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 gcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggca 1440


Query: 1644 gtgaccaaacagcctaaatccgaagctggggataccagcctctaa 1688
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 gtgaccaaacagcctaaatccgaagctggggataccagcctctaa 1485
```

>gi|32261308|ref|NM_022571.3| LUG Homo sapiens G protein-coupled receptor 135 (G
Length = 1485

Score = 2920 bits (1473), Expect = 0.0
Identities = 1400/1485 (94%)
Strand = Plus / Plus

```
Query: 204  atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 263
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    atggaggagccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcac 60


Query: 264  tccggcgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggcc 323
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   tccggcgccccctccgcggccggcccacctggcgggacttcctccgcggccacggcggcc 120


Query: 324  gtgctctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcgga 383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gtgctctccttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcgga 180


Query: 384  ggcggcacagctgccgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 443
            ||||||||||||||||||
```

```
Sbjct: 181  ggcggcacagctgccgctcccggtggcggcggccttggcgggtccggggcagcgcgggag 240

Query: 444  nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacgga 503
                                                        ||||||||||||||||||
Sbjct: 241  gcgggggcggcggtgaggcggccgctaggcccggaggcggcgccgctgctgtcgcacgga 300

Query: 504  gctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggc 563
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  gctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggc 360

Query: 564  aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 623
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  aactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgcc 420

Query: 624  ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgcc 683
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgcc 480

Query: 684  ttcctggacctcttcactccgccccgggggttcggcgcctgccgccgccgcggggccctgg 743
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  ttcctggacctcttcactccgccccgggggttcggcgcctgccgccgccgcggggccctgg 540

Query: 744  cgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 803
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  cgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtccacgctc 600

Query: 804  agcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaag 863
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  agcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaag 660

Query: 864  atcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttc 923
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  atcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttc 720

Query: 924  tccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccac 983
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  tccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccac 780

Query: 984  ggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtgggg 1043
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtgggg 840

Query: 1044 ctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatc 1103
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  ctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatc 900

Query: 1104 tgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 1163
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 901  tgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtg 960

Query: 1164 ctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1223
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961  ctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtc 1020

Query: 1224 atctgctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccag 1283
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 atctgctgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccag 1080

Query: 1284 accatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggg 1343
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081 accatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggg 1140

Query: 1344 gccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgc 1403
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 gccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgc 1200

Query: 1404 aaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccg 1463
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 aaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccg 1260

Query: 1464 ggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcc 1523
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 ggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcc 1320

Query: 1524 tgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgg 1583
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 tgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgg 1380

Query: 1584 gcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggca 1643
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 gcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagccggtgacggca 1440

Query: 1644 gtgaccaaacagcctaaatccgaagctggggataccagcctctaa 1688
             ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 gtgaccaaacagcctaaatccgaagctggggataccagcctctaa 1485
```

>gi|2810988|gb|M76676.1|HUMNPIIY20 LUG Homo sapiens leukocyte platelet-activatin complete cds
Length = 1481

Score = 2700 bits (1362), Expect = 0.0
Identities = 1384/1489 (92%), Gaps = 10/1489 (0%)
Strand = Plus / Plus

```
Query: 152  ggccgccgcccccggtgcgggatgaggagatccgcggccgccactgggccccatggagga 211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 1    ggccgccgcccccggtgcgggatgaggagatccgcggccgccactgggccccatggagga 60

Query: 212  gccgcagccgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgc 271
             |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   gccgccgccgccccgcccaccagcgagcatggccttactgggcagccagcactccggcgc 120

Query: 272  cccctccgcggccggcccacctggcgggacttcctccgcggccacggcggccgtgctctc 331
             |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 121  cccctccgcggccggcccacctggcgggacttcctcagcggccacggcggccgtgctctc 180

Query: 332  cttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcggcac 391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  cttcagcaccgtggcgaccgcggcgctggggaacctgagcgacgcaagcggaggcggcac 240

Query: 392  agctgccgcnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 451
             |||||||||
Sbjct: 241  agctgccgctcccggtggcggcggccttggcgggtccggggcagcgcgggaggcgggggc 300

Query: 452  nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccgctgctgtcgcacggagctgcagt 511
                                              ||||||||||||||||||||||||
Sbjct: 301  ggcggtgaggcggccgctaggcccggaggcggcgccgctgctgtcgcacggagctgcagt 360

Query: 512  ggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactgcgc 571
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  ggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagccttggcaactgcgc 420

Query: 572  ggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcatcct 631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcaccaacgccttcatcct 480

Query: 632  gtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcctgga 691
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  gtcgctgtccctatcggatctgctcacggcgctgctctgcctgcccgccgccttcctgga 540

Query: 692  cctcttcactccgcccgggggttcggcgcctgccgccg-ccgcggggccctggcgcggct 750
             |||||||||||||||||||||||||||||| ||| | ||||||||||||||||||||
Sbjct: 541  cctcttcactccgcccgggggttcggcgcctg-cgctgcccgcggggccctggcgcggct 599

Query: 751  tctgcgccgcc-agccgcttcttcagctcgtgcttcggcatcgtgtccacgctcagcgtg 809
             ||||| | ||| ||||||||||||||||||||||||||||||  ||||||||||||
Sbjct: 600  tctgc-cggccaagccgcttcttcagctcgtgcttcggcatcgtgt--acgctcagcgtg 656

Query: 810  gcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgggagaagatcggc 869
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 657  gcgctcatctcgttggaccgttactgcgctatcgt-cggccgccgcgggagaagatcggc 715

Query: 870  cgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttctccttg 929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 716  cgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctgggcttctccttg 775

Query: 930  ccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagcttccacggctgc 989
             ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Sbjct: 776  ccctgggagctgctcggggcgccccgggaactcgcggcgggccagagcttccacggctgc 835

Query: 990  ctctaccggacctccccggaccccgcgcagctgggcgcggccttcagcgtggggctggtg 1049
             ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Sbjct: 836  ctctaccggacctccccggaccccgcgcagctgggcggcccccttcagcgtggggctggtg 895

Query: 1050 gtggcctgctacctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaag 1109
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct: 896  gtggcctgctacctgctgcccttcctgctcatctgcttctgccactaccacatctgcaag 955

Query: 1110 acggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcgc 1169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 956  acggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcg- 1014

Query: 1170 ttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgc 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1015 ttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgc 1074

Query: 1230 tgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccagaccatg 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1075 tgctgggggccctactgcttcctggtgctgctggccgccgcccggcaggcccagaccatg 1134

Query: 1290 caggcccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatc 1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1135 caggcccccctcgctcctcagcgtggtggccgtctggctgacctgggccaatggggccatc 1194

Query: 1350 aaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgc 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1195 aaccctgtcatctacgccatccgcaatcccaacatttcgatgctcctagggcgcaaccgc 1254

Query: 1410 gaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccgggtctg 1469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1255 gaggagggctaccggactaggaatgtggacgctttcctgcccagccagggcccgggtctg 1314

Query: 1470 caagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaac 1529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1315 caagccagaagccgcagtcgccttcgaaaccgctatgccaaccggctgggggcctgcaac 1374

Query: 1530 aggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtgggcccgc 1589
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 1375 aggatgtcctcttccaacccggccagcggagtggcaggggacgtggccatgtggg-ccgc 1433

Query: 1590 aaaaatccagttgtacttttctgccgagagggaccaccagagccggtga 1638
              |||||||||||||||||||||||||||| ||||||||||||||||||
```

```
Sbjct: 1434 aaaaatccagttgtacttttctgccgaga-ggaccaccagagccggtga 1481
```

>gi|29611577|gb|AY255588.1| LU Homo sapiens leukocyte platelet-activating factor partial cds
Length = 546

```
 Score = 1082 bits (546), Expect = 0.0
 Identities = 546/546 (100%)
 Strand = Plus / Plus

Query: 498  cacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagc 557
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    cacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttcctgctgtctagc 60

Query: 558  cttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcacc 617
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   cttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctccgcaccgtcacc 120

Query: 618  aacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgccc 677
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  aacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctgctctgcctgccc 180

Query: 678  gccgccttcctggacctcttcactccgcccgggggttcggcgcctgccgccgccgcgggg 737
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  gccgccttcctggacctcttcactccgcccgggggttcggcgcctgccgccgccgcgggg 240

Query: 738  ccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtcc 797
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  ccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtgtcc 300

Query: 798  acgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgg 857
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  acgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccgcgg 360

Query: 858  gagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctg 917
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  gagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggccctg 420

Query: 918  ggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagc 977
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcagagc 480

Query: 978  ttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagc 1037
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  ttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttcagc 540

Query: 1038 gtgggg 1043
            ||||||
```

```
Sbjct: 541  gtgggg 546
```

>gi|38565931|gb|BC062104.1| Mus musculus cDNA clone IMAGE:6809932, with apparent
Length = 3076

```
 Score =  803 bits (405), Expect = 0.0
 Identities = 771/893 (86%)
 Strand = Plus / Plus

Query: 735  gggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtg 794
            ||||||||||||| |||||||||| |||||||||||||||||| ||||| ||||| |||||
Sbjct: 454  gggccctggcgcagcttctgcgcagccagccgcttcttcagttcgtgtttcggaatcgta 513

Query: 795  tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccg 854
            |||||| |||||||||||||||||||| ||||||| |||||||| ||||||||||||||
Sbjct: 514  tccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgccg 573

Query: 855  cgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggcc 914
            ||||| ||| | ||||| || ||||||||||||||||||| || || ||| || | ||
Sbjct: 574  cgggacaagctgggccggcggcgcgcgctgcagctgctggcaggagcgtggttggctgcg 633

Query: 915  ctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcag 974
            |||||||||||| |||||||||| |||||| |||| |||||||| | | | ||  |||||
Sbjct: 634  ctgggcttctccctgccctgggacctgctcagggcaccccgggagccccccgctccgcag 693

Query: 975  agcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttc 1034
            ||||||||| ||||||| ||| | |||||||| ||||| ||||||||||||  |||| |
Sbjct: 694  agcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgtcgcctac 753

Query: 1035 agcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccac 1094
          |||||||| |||||||||| |||||| |||||||||||| || ||||| ||||||| |
Sbjct: 754  agcgtgggactggtggtggcttgctacttgctgcccttcctactgatgtgtttctgccgc 813

Query: 1095 taccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154
          |||||||||||||||| |||||||||||||||||||||||||||||| ||| ||| |||
Sbjct: 814  taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 873

Query: 1155 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatc 1214
          ||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Sbjct: 874  gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccaccgtgctcatcatgatt 933

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgcccgg 1274
           |||| ||||| |||||||||| ||||||||||||||||||||||||||||  |||||
Sbjct: 934  atctttgtcatgtgctgctggggtccctactgcttcctggtgctgctggccgcgacccgg 993

Query: 1275 caggcccagaccatgcaggcccccctcgctcctcagcgtggtggccgtctggctgacctgg 1334
          ||||  ||| ||| |||||| |||||||| |||| |||| ||| || ||||||||||||
Sbjct: 994  cagggtcaggccacgcaggctccctcgctgctcaatgtggcggctgtttggctgacctgg 1053
```

```
Query: 1335 gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394
           |||||||||||| |||||||| ||||| || |||||||||||| |||||||||||| ||||||
Sbjct: 1054 gccaatggggctatcaacccggtcatatatgccatccgcaaccccaacatttccatgctc 1113


Query: 1395 ctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagc 1454
           ||||| |||||||||||| || || ||| ||||||| ||  |||| |||||  |||| |||
Sbjct: 1114 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgctttttgcctagc 1173


Query: 1455 cagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514
           || ||||  ||| | |||||||||||| |||| ||||||||||||  ||| ||||||| ||
Sbjct: 1174 caaggcctaggttttcaagccagaagtcgcaatcgccttcgaaatggctgtgccaacagg 1233


Query: 1515 ctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtg 1574
           || ||||| |||| ||||||| | |||||||||||| || || ||    | |||||| |||
Sbjct: 1234 cttggggcttgcagcaggatgccttcttccaacccagctagtgggtcaggaggggaagtg 1293


Query: 1575 gccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccacc 1627
           | ||||||||| || |||||||||||||| || |||| ||||||||| |||||
Sbjct: 1294 gtcatgtgggctcgaaaaaatccagttgtgctcttcttccgagagggtccacc 1346
```

Score = 260 bits (131), Expect = 9e-66
Identities = 185/203 (91%)
Strand = Plus / Plus

```
Query: 486 ccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttc 545
           |||||||| | |||||| || || ||||| |||||||||||||| ||||||||||||||
Sbjct: 223 ccgctgctatggcacggggcagcggtggccgcccaggcgctcgtgctcctgctcatcttc 282


Query: 546 ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605
           |||||||||||||| ||||||||||||||||||||||||||| |||||||| ||||||||
Sbjct: 283 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 342


Query: 606 cgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctg 665
           ||||| ||||| |||||||||||||||||||||||||| ||||| |||||||| ||||||
Sbjct: 343 cgcacggtcacaaacgccttcatcctgtcgctgtccctgtcggacctgctcactgcgctg 402


Query: 666 ctctgcctgcccgccgccttcct 688
           |||||||| ||||||||||||||
Sbjct: 403 ctctgcctacccgccgccttcct 425
```

>gi|32165533|gb|AY288425.1| LU Mus musculus G protein-coupled receptor 135 (Gpr13
cds
Length = 1374

Score = 803 bits (405), Expect = 0.0
Identities = 771/893 (86%)

Strand = Plus / Plus

```
Query: 735  gggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtg 794
            ||||||||||||| |||||||||| |||||||||||||||| ||||| ||||| |||||
Sbjct: 421  gggccctggcgcagcttctgcgcagccagccgcttcttcagttcgtgtttcggaatcgta 480

Query: 795  tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccg 854
            |||||| |||||||||||||||||| ||||||| |||||||| ||||||||||||||
Sbjct: 481  tccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgccg 540

Query: 855  cgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggcc 914
            ||||| ||| | ||||| || ||||||||||||||||||| || || ||| || | ||
Sbjct: 541  cgggacaagctgggccggcggcgcgcgctgcagctgctggcaggagcgtggttggctgcg 600

Query: 915  ctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcag 974
            |||||||||||| |||||||||| |||||| |||| |||||||| | | | ||  |||||
Sbjct: 601  ctgggcttctccctgccctgggacctgctcagggcaccccgggagccccccgctccgcag 660

Query: 975  agcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttc 1034
            ||||||||| ||||||| ||| | |||||||| ||||| |||||||||||||  |||| |
Sbjct: 661  agcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgtcgcctac 720

Query: 1035 agcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccac 1094
            |||||||| |||||||||| |||||| |||||||||||| || ||||| ||||||| |
Sbjct: 721  agcgtgggactggtggtggcttgctacttgctgcccttcctactgatgtgtttctgccgc 780

Query: 1095 taccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154
            |||||||||||||||| |||||||||||||||||||||||||||| ||| ||| |||
Sbjct: 781  taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 840

Query: 1155 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatc 1214
            |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Sbjct: 841  gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccaccgtgctcatcatgatt 900

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgcccgg 1274
             |||| ||||| |||||||||| |||||||||||||||||||||||||||||  |||||
Sbjct: 901  atctttgtcatgtgctgctggggtccctactgcttcctggtgctgctggccgcgacccgg 960

Query: 1275 caggcccagaccatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgg 1334
            ||||  ||| ||| |||||| |||||||| ||||  |||| ||| || ||||||||||||
Sbjct: 961  cagggtcaggccacgcaggctccctcgctgctcaatgtggcggctgtttggctgacctgg 1020

Query: 1335 gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394
            |||||||||| |||||||| ||||| || |||||||||| |||||||||| ||||||
Sbjct: 1021 gccaatggggctatcaacccggtcatatatgccatccgcaaccccaacatttccatgctc 1080

Query: 1395 ctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagc 1454
            ||||| |||||||||| || || ||| ||||||| ||  |||| |||||  |||| |||
```

```
Sbjct: 1081 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgctttttgcctagc 1140


Query: 1455 cagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514
            || ||||  ||| | ||||||||||| |||| |||||||||||  ||| ||||||| ||
Sbjct: 1141 caaggcctaggttttcaagccagaagtcgcaatcgccttcgaaatggctgtgccaacagg 1200


Query: 1515 ctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtg 1574
            || ||||| |||| ||||||| | |||||||||| || || ||    | |||||| |||
Sbjct: 1201 cttggggcttgcagcaggatgccttcttccaacccagctagtgggtcaggaggggaagtg 1260


Query: 1575 gccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccacc 1627
            | ||||||||| || |||||||||||||| || |||| ||||||||| |||||
Sbjct: 1261 gtcatgtgggctcgaaaaaatccagttgtgctcttcttccgagagggtccacc 1313


 Score =  260 bits (131), Expect = 9e-66
 Identities = 185/203 (91%)
 Strand = Plus / Plus


Query: 486 ccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttc 545
            |||||||| | |||||| || || ||||| |||||||||||||| ||||||||||||||
Sbjct: 190 ccgctgctatggcacggggcagcggtggccgcccaggcgctcgtgctcctgctcatcttc 249


Query: 546 ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605
            |||||||||||| |||||||||||||||||||||||||| |||||||| ||||||||
Sbjct: 250 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 309


Query: 606 cgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctg 665
            ||||| ||||| |||||||||||||||||||||||||| ||||| |||||||| ||||||
Sbjct: 310 cgcacggtcacaaacgccttcatcctgtcgctgtccctgtcggacctgctcactgcgctg 369


Query: 666 ctctgcctgcccgccgccttcct 688
            |||||||| ||||||||||||||
Sbjct: 370 ctctgcctacccgccgccttcct 392


>gi|32964966|gb|AC110170.6|  Mus musculus chromosome 12, clone RP23-301G24, compl
          Length = 173081

 Score =  803 bits (405), Expect = 0.0
 Identities = 771/893 (86%)
 Strand = Plus / Minus


Query: 735   gggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtg 794
            |||||||||||| |||||||||| |||||||||||||||| ||||| ||||| |||||
Sbjct: 35355 gggccctggcgcagcttctgcgcagccagccgcttcttcagttcgtgtttcggaatcgta 35296


Query: 795   tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccg 854
            |||||| |||||||||||||||||||| ||||||| |||||||| ||||||||||||||
```

```
Sbjct: 35295 tccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgccg 35236

Query: 855   cgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggcc 914
              ||||| ||| | ||||| || ||||||||||||||||||||| || || ||| || | ||
Sbjct: 35235 cgggacaagctgggccggcggcgcgcgctgcagctgctggcaggagcgtggttggctgcg 35176

Query: 915   ctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcag 974
              |||||||||||| |||||||||| |||||| |||| |||||||| | | | ||  |||||
Sbjct: 35175 ctgggcttctccctgccctgggacctgctcagggcaccccgggagccccccgctccgcag 35116

Query: 975   agcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttc 1034
              ||||||||| ||||||| ||| | |||||||| ||||| |||||||||||||  |||| |
Sbjct: 35115 agcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgtcgcctac 35056

Query: 1035  agcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccac 1094
              |||||||| |||||||||| |||||| |||||||||||| || ||||| ||||||| |
Sbjct: 35055 agcgtgggactggtggtggcttgctacttgctgcccttcctactgatgtgtttctgccgc 34996

Query: 1095  taccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154
              |||||||||||||||| |||||||||||||||||||||||||||| ||| ||| |||
Sbjct: 34995 taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 34936

Query: 1155  gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatc 1214
              |||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Sbjct: 34935 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccaccgtgctcatcatgatt 34876

Query: 1215  gtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgcccgg 1274
               |||| ||||| |||||||||| |||||||||||||||||||||||||||  |||||
Sbjct: 34875 atctttgtcatgtgctgctggggtccctactgcttcctggtgctgctggccgcgacccgg 34816

Query: 1275  caggcccagaccatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgg 1334
              ||||  ||| ||| |||||| |||||||| |||| |||| ||| || ||||||||||||
Sbjct: 34815 cagggtcaggccacgcaggctccctcgctgctcaatgtggcggctgtttggctgacctgg 34756

Query: 1335  gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394
              |||||||||| |||||||| ||||| || |||||||||| |||||||||| ||||||
Sbjct: 34755 gccaatggggctatcaacccggtcatatatgccatccgcaaccccaacatttccatgctc 34696

Query: 1395  ctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagc 1454
              ||||| |||||||||| || || ||| ||||||| ||  |||| |||||  |||| |||
Sbjct: 34695 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgctttttgcctagc 34636

Query: 1455  cagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514
              || ||||  ||| | |||||||||| |||| |||||||||||  ||| ||||||| ||
Sbjct: 34635 caaggcctaggttttcaagccagaagtcgcaatcgccttcgaaatggctgtgccaacagg 34576

Query: 1515  ctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtg 1574
              || ||||| |||| ||||||| | |||||||||| || || ||    | |||||| |||
```

```
Sbjct: 34575 cttggggcttgcagcaggatgccttcttccaacccagctagtgggtcaggaggggaagtg 34516


Query: 1575  gccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccacc 1627
              | |||||||||  || ||||||||||||||  || ||||  |||||||||  |||||
Sbjct: 34515 gtcatgtgggctcgaaaaaatccagttgtgctcttcttccgagagggtccacc 34463


 Score =  260 bits (131), Expect = 9e-66
 Identities = 185/203 (91%)
 Strand = Plus / Minus


Query: 486   ccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttc 545
              ||||||||  | ||||||  ||  ||  |||||  ||||||||||||||  ||||||||||||||
Sbjct: 35586 ccgctgctatggcacggggcagcggtggccgcccaggcgctcgtgctcctgctcatcttc 35527


Query: 546   ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605
               ||||||||||||  |||||||||||||||||||||||||||  ||||||||  ||||||||
Sbjct: 35526 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 35467


Query: 606   cgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctg 665
              |||||  ||||||  ||||||||||||||||||||||||||  |||||  ||||||||  ||||||
Sbjct: 35466 cgcacggtcacaaacgccttcatcctgtcgctgtccctgtcggacctgctcactgcgctg 35407


Query: 666   ctctgcctgcccgccgccttcct 688
              ||||||||  ||||||||||||||
Sbjct: 35406 ctctgcctacccgccgccttcct 35384


 Score = 58.0 bits (29), Expect = 7e-05
 Identities = 45/49 (91%), Gaps = 1/49 (2%)
 Strand = Plus / Minus


Query: 4     tcctgcgtaaacacgcggttccctcggcaacgc-tggaacccacgtcaa 51
              ||||||||||||  | |||||||||||||||||||  | ||||||||||||||
Sbjct: 35943 tcctgcgtaaataggcggttccctcggcaacgcctagaacccacgtcaa 35895


>gi|32306523|ref|NM_181752.1|  LU Mus musculus G protein-coupled receptor 135 (Gpr
          Length = 1374

 Score =  803 bits (405), Expect = 0.0
 Identities = 771/893 (86%)
 Strand = Plus / Plus


Query: 735  gggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcgtg 794
             ||||||||||||  ||||||||||  ||||||||||||||||  |||||  |||||  |||||
Sbjct: 421  gggccctggcgcagcttctgcgcagccagccgcttcttcagttcgtgtttcggaatcgta 480


Query: 795  tccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgccg 854
```

```
            |||||| |||||||||||||||||||| ||||||| |||||||| ||||||||||||||||
Sbjct: 481  tccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgccg 540

Query: 855  cgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacggcc 914
            |||||| ||| | |||||| || |||||||||||||||||||| || || ||| || | ||
Sbjct: 541  cgggacaagctgggccggcggcgcgcgctgcagctgctggcaggagcgtggttggctgcg 600

Query: 915  ctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgcag 974
            |||||||||||| |||||||||| |||||| |||| |||||||| | | | ||  ||||| 
Sbjct: 601  ctgggcttctccctgccctgggacctgctcagggcaccccgggagccccccgctccgcag 660

Query: 975  agcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggccttc 1034
            ||||||||| ||||||| ||| | |||||||| ||||| |||||||||||||  |||| | 
Sbjct: 661  agcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgtcgcctac 720

Query: 1035 agcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgccac 1094
            |||||||| |||||||||| |||||| |||||||||||| || ||||| ||||||| | 
Sbjct: 721  agcgtgggactggtggtggcttgctacttgctgcccttcctactgatgtgtttctgccgc 780

Query: 1095 taccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacctac 1154
            |||||||||||||||| |||||||||||||||||||||||||||| ||| ||| |||
Sbjct: 781  taccacatctgcaagaccgtgcgcctgtcggacgtgcgcgtgcggccgatgaccacttac 840

Query: 1155 gcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatgatc 1214
            |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||
Sbjct: 841  gcgcgcgtgctgcgcttcttcagcgaggtgcgcacagccaccaccgtgctcatcatgatt 900

Query: 1215 gtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgcccgg 1274
             |||| ||||| |||||||||| |||||||||||||||||||||||||||  |||||
Sbjct: 901  atctttgtcatgtgctgctggggtccctactgcttcctggtgctgctggccgcgacccgg 960

Query: 1275 caggcccagaccatgcaggccccctcgctcctcagcgtggtggccgtctggctgacctgg 1334
            ||||  ||| ||| |||||| |||||||| |||| |||| ||| || ||||||||||||
Sbjct: 961  cagggtcaggccacgcaggctccctcgctgctcaatgtggcggctgtttggctgacctgg 1020

Query: 1335 gccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgctc 1394
            |||||||||| |||||||| ||||| || |||||||||| |||||||||| |||||||
Sbjct: 1021 gccaatggggctatcaacccggtcatatatgccatccgcaaccccaacatttccatgctc 1080

Query: 1395 ctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgcccagc 1454
            ||||| |||||||||| || || ||| ||||||| ||  |||| |||||  |||| |||
Sbjct: 1081 ctaggacgcaaccgcgaagaagggtacaggactagaaacatggatgctttttgcctagc 1140

Query: 1455 cagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaaccgg 1514
            || ||||  ||| | |||||||||||| |||| ||||||||||||  ||| ||||||| ||
Sbjct: 1141 caaggcctaggttttcaagccagaagtcgcaatcgccttcgaaatggctgtgccaacagg 1200

Query: 1515 ctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacgtg 1574
```

```
           || ||||| |||| ||||||| | |||||||||||| || || ||    | |||||| |||
Sbjct: 1201 cttggggcttgcagcaggatgccttcttccaacccagctagtgggtcaggaggggaagtg 1260


Query: 1575 gccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccacc 1627
           | ||||||||| || |||||||||||||| || |||| ||||||||| |||||
Sbjct: 1261 gtcatgtgggctcgaaaaaatccagttgtgctcttcttccgagagggtccacc 1313


 Score =  260 bits (131), Expect = 9e-66
 Identities = 185/203 (91%)
 Strand = Plus / Plus


Query: 486 ccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctcatcttc 545
           |||||||| | |||||| || || ||||| |||||||||||||| ||||||||||||||
Sbjct: 190 ccgctgctatggcacggggcagcggtggccgcccaggcgctcgtgctcctgctcatcttc 249


Query: 546 ctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggcagctc 605
           |||||||||||||| |||||||||||||||||||||||||| |||||||| ||||||||
Sbjct: 250 ttgctgtctagcctgggcaactgcgcggtgatgggggtgatcgtgaagcatcggcagctg 309


Query: 606 cgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacggcgctg 665
           ||||| ||||| |||||||||||||||||||||||||| ||||| |||||||| ||||||
Sbjct: 310 cgcacggtcacaaacgccttcatcctgtcgctgtccctgtcggacctgctcactgcgctg 369


Query: 666 ctctgcctgcccgccgccttcct 688
           |||||||| ||||||||||||||
Sbjct: 370 ctctgcctacccgccgccttcct 392
```

>gi|32165543|gb|AY288430.1| LU Rattus norvegicus G protein-coupled receptor 135 (complete cds
Length = 1374

```
 Score =  783 bits (395), Expect = 0.0
 Identities = 797/931 (85%)
 Strand = Plus / Plus


Query: 733  cggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcg 792
            |||||||||||||| |||||||||||||||||||||||||||| ||||| ||||||||||
Sbjct: 419  cggggccctggcgcagcttctgcgccgccagccgcttcttcagttcgtgtttcggcatcg 478


Query: 793  tgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgc 852
            | |||||| |||||||||||||||||| ||||||| |||||||| ||||||||||||
Sbjct: 479  tctccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgc 538


Query: 853  cgcgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacgg 912
            ||||||| ||| | ||||| || |||||||||||||||||| || || |||||| | |
Sbjct: 539  cgcgggacaagctaggccggcggcgcgcgctgcagctgctggccggagcgtggctggctg 598
```

```
Query: 913  ccctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgc 972
            | || ||||||||| |||||||||||||||| |||| |||||||| | | || |  |||
Sbjct: 599  cgctcggcttctccctgccctgggagctgctccgggcaccccgggagcccccgactccgc 658

Query: 973  agagcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggcct 1032
            |||||||||||| ||||||| ||| | |||||||| ||||| |||||||||||||| || |
Sbjct: 659  agagcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgccgctt 718

Query: 1033 tcagcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgcc 1092
             |||||||||||||||||||| |||||||||||||||||||||| ||||| |||||||
Sbjct: 719  acagcgtggggctggtggtggcttgctacctgctgcccttcctgctgatgtgtttctgcc 778

Query: 1093 actaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacct 1152
             |||||||||||||||||| |||||||||||||||||||| ||||||||| ||| |||||
Sbjct: 779  gctaccacatctgcaagactgtgcgcctgtcggacgtgcgtgtgcggccgatgaccacct 838

Query: 1153 acgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatga 1212
            | |||||||||||||||| |||||||||||||||||||||||||||| ||||||||||
Sbjct: 839  atgcgcgcgtgctgcgctttttcagcgaggtgcgcacggccaccaccgtgctcatcatga 898

Query: 1213 tcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgccc 1272
            | ||||| |||||||||||||||| |||||||||||||||||| || |||| ||  |||
Sbjct: 899  ttgtctttgtcatctgctgctggggcccctactgcttcctggtgttgttggctgctaccc 958

Query: 1273 ggcaggcccagaccatgcaggccccctcgctcctcagcgtggtggccgtctggctgacct 1332
            ||||||  |||||||  ||||| |||||||| ||||  ||||  || || ||||||||||
Sbjct: 959  ggcagggtcagaccacacaggctccctcgctgctcaatgtggcagctgtttggctgacct 1018

Query: 1333 gggccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgc 1392
            |||||||||| || |||||||| ||||| || |||||||||| || |||||||| |||
Sbjct: 1019 gggccaatggagctatcaacccggtcatatatgccatccgcaaccctaacatttctatgt 1078

Query: 1393 tcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgccca 1452
            ||||||| |||||||||| ||||| ||  ||||||| ||  |||| | |||  |||| |
Sbjct: 1079 tcctaggtcgcaaccgcgaagagggatataggactagaaacatggatgtttttttgcctа 1138

Query: 1453 gccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaacc 1512
            |||| ||||  ||| | || |||||||| |||| |||||||||||  ||| ||||||||
Sbjct: 1139 gccaaggcctaggttttcaggccagaagtcgcaatcgccttcgaaatggctgtgccaaca 1198

Query: 1513 ggctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacg 1572
            |||| ||||| |||| ||||||| | |||||||||| || || ||    | |||||| |
Sbjct: 1199 ggcttggggcttgcagcaggatgccttcttccaaccccgctagtgggtcaggaggggaag 1258

Query: 1573 tggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagc 1632
            ||| ||||||||| || ||||| |||||||| || |||| ||||||||  |||||||| |
Sbjct: 1259 tggtcatgtgggctcgaaaaaacccagttgtgctcttcttccgagaggatccaccagacc 1318
```

```
Query: 1633 cggtgacggcagtgaccaaacagcctaaatc 1663
           | || | ||||||   |||||||| ||||||
Sbjct: 1319 cagttatggcagtctacaaacagcataaatc 1349
```

Score = 258 bits (130), Expect = 3e-65
Identities = 189/214 (88%)
Strand = Plus / Plus

```
Query: 481 nnnnnccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 540
           ||||||||  | ||||||  || ||||||||  ||||||||||||||  ||||||||||
Sbjct: 185 cggcaccgctgctttggcacggggcagcagtggccgcccaggcgctcgtgctcctgctca 244

Query: 541 tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600
           |||||  | ||||||||||  || ||||||||||||||||||||||  ||||||||||||
Sbjct: 245 tcttcttactgtctagcctgggaaactgcgcggtgatgggggtgatcgtgaagcaccggc 304

Query: 601 agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 660
           ||||  |||||  ||||||||||||||||||||  ||||||||||  |||||  |||||||  |
Sbjct: 305 agctgcgcacggtcaccaacgccttcatcctatcgctgtccctgtcggacctgctcactg 364

Query: 661 cgctgctctgcctgcccgccgccttcctggacct 694
           ||||||||||  | ||||||||||||||  |||||
Sbjct: 365 cgctgctctgcttacccgccgccttcctcgacct 398
```

>gi|32401462|ref|NM_181771.1| LU Rattus norvegicus G protein-coupled receptor 135
Length = 1374

Score = 783 bits (395), Expect = 0.0
Identities = 797/931 (85%)
Strand = Plus / Plus

```
Query: 733  cggggccctggcgcggcttctgcgccgccagccgcttcttcagctcgtgcttcggcatcg 792
           ||||||||||||||  |||||||||||||||||||||||||||||||  |||||  ||||||||||
Sbjct: 419  cggggccctggcgcagcttctgcgccgccagccgcttcttcagttcgtgtttcggcatcg 478

Query: 793  tgtccacgctcagcgtggcgctcatctcgttggaccgttactgcgctatcgtgcggccgc 852
           |  ||||||  ||||||||||||||||||||  |||||||  ||||||||  ||||||||||||
Sbjct: 479  tctccacgttcagcgtggcgctcatctcgctggaccgctactgcgccatcgtgcggccgc 538

Query: 853  cgcgggagaagatcggccgccgccgcgcgctgcagctgctggcgggcgcctggctgacgg 912
           |||||||  |||  |  |||||  ||  ||||||||||||||||||||  ||  ||  ||||||  |  |
Sbjct: 539  cgcgggacaagctaggccggcggcgcgcgctgcagctgctggccggagcgtggctggctg 598

Query: 913  ccctgggcttctccttgccctgggagctgctcggggcgccccgggaactcgcggcggcgc 972
           |  ||  |||||||||  ||||||||||||||||  ||||  ||||||||  |  |  ||  |  |||
Sbjct: 599  cgctcggcttctccctgccctgggagctgctccgggcaccccgggagcccccgactccgc 658
```

```
Query: 973  agagcttccacggctgcctctaccggacctccccggaccccgcgcagctgggcgcggcct 1032
            |||||||||||| ||||||| ||| | |||||||| ||||| ||||||||||||| || |
Sbjct: 659  agagcttccaccgctgcctttacagaacctccccagaccctgcgcagctgggcgccgctt 718

Query: 1033 tcagcgtggggctggtggtggcctgctacctgctgcccttcctgctcatgtgcttctgcc 1092
             ||||||||||||||||||| |||||||||||||||||||||| ||||| |||||||
Sbjct: 719  acagcgtggggctggtggtggcttgctacctgctgcccttcctgctgatgtgtttctgcc 778

Query: 1093 actaccacatctgcaagacggtgcgcctgtcggacgtgcgcgtgcggccggtgaacacct 1152
             |||||||||||||||||| |||||||||||||||||||| ||||||||| ||| |||||
Sbjct: 779  gctaccacatctgcaagactgtgcgcctgtcggacgtgcgtgtgcggccgatgaccacct 838

Query: 1153 acgcgcgcgtgctgcgcttcttcagcgaggtgcgcacggccaccaccgtcctcatcatga 1212
             | |||||||||||||||| |||||||||||||||||||||||||||| ||||||||||
Sbjct: 839  atgcgcgcgtgctgcgctttttcagcgaggtgcgcacggccaccaccgtgctcatcatga 898

Query: 1213 tcgtcttcgtcatctgctgctgggggccctactgcttcctggtgctgctggccgccgccc 1272
             | ||||| |||||||||||||||| |||||||||||||||| || |||| ||  |||
Sbjct: 899  ttgtctttgtcatctgctgctgggggcccctactgcttcctggtgttgttggctgctaccc 958

Query: 1273 ggcaggcccagaccatgcaggcccccctcgctcctcagcgtggtggccgtctggctgacct 1332
             ||||||  |||||||  |||||  |||||||| ||||  ||||  || || ||||||||||
Sbjct: 959  ggcagggtcagaccacacaggctccctcgctgctcaatgtggcagctgtttggctgacct 1018

Query: 1333 gggccaatggggccatcaaccctgtcatctacgccatccgcaatcccaacatttcgatgc 1392
             |||||||||| || |||||||| ||||| || |||||||||| || |||||||| |||
Sbjct: 1019 gggccaatggagctatcaacccggtcatatatgccatccgcaaccctaacatttctatgt 1078

Query: 1393 tcctagggcgcaaccgcgaggagggctaccggactaggaatgtggacgctttcctgccca 1452
             ||||||| |||||||||| ||||| ||  ||||||| ||  |||| | |||  |||| |
Sbjct: 1079 tcctaggtcgcaaccgcgaagagggatataggactagaaacatggatgttttttgcctа 1138

Query: 1453 gccagggcccgggtctgcaagccagaagccgcagtcgccttcgaaaccgctatgccaacc 1512
             |||| ||||  ||| | || |||||||| |||| |||||||||||  ||| |||||||
Sbjct: 1139 gccaaggcctaggttttcaggccagaagtcgcaatcgccttcgaaatggctgtgccaaca 1198

Query: 1513 ggctgggggcctgcaacaggatgtcctcttccaacccggccagcggagtggcaggggacg 1572
             |||| ||||| |||| ||||||| | |||||||||| || || ||    | |||||| |
Sbjct: 1199 ggcttggggcttgcagcaggatgccttcttccaaccccgctagtgggtcaggaggggaag 1258

Query: 1573 tggccatgtgggcccgcaaaaatccagttgtacttttctgccgagagggaccaccagagc 1632
             ||| ||||||||| || ||||| |||||||| || |||| |||||||| ||||||||
Sbjct: 1259 tggtcatgtgggctcgaaaaaacccagttgtgctcttcttccgagaggatccaccagacc 1318

Query: 1633 cggtgacggcagtgaccaaacagcctaaatc 1663
             | || | ||||||   |||||||| ||||||
Sbjct: 1319 cagttatggcagtctacaaacagcataaatc 1349
```

```
 Score =  258 bits (130), Expect = 3e-65
 Identities = 189/214 (88%)
 Strand = Plus / Plus


Query: 481 nnnnnccgctgctgtcgcacggagctgcagtggcggcccaggcgctcgtcctcctgctca 540
               |||||||| | |||||| || |||||||| ||||||||||||||| |||||||||
Sbjct: 185 cggcaccgctgctttggcacggggcagcagtggccgcccaggcgctcgtgctcctgctca 244


Query: 541 tcttcctgctgtctagccttggcaactgcgcggtgatgggggtgattgtgaagcaccggc 600
           ||||| | |||||||||||| || ||||||||||||||||||||||| ||||||||||||
Sbjct: 245 tcttcttactgtctagcctgggaaactgcgcggtgatgggggtgatcgtgaagcaccggc 304


Query: 601 agctccgcaccgtcaccaacgccttcatcctgtcgctgtccctatcggatctgctcacgg 660
           |||| ||||| |||||||||||||||||| |||||||||| ||||| |||||||| |
Sbjct: 305 agctgcgcacggtcaccaacgccttcatcctatcgctgtccctgtcggacctgctcactg 364


Query: 661 cgctgctctgcctgcccgccgccttcctggacct 694
           |||||||||||| | ||||||||||||| |||||
Sbjct: 365 cgctgctctgcttacccgccgccttcctcgacct 398
```

>gi|32563165|emb|BX004994.6| D Zebrafish DNA sequence from clone DKEY-24J15 in lin
complete sequence
Length = 211945

```
 Score =  137 bits (69), Expect = 9e-29
 Identities = 159/189 (84%)
 Strand = Plus / Minus


Query: 1059  tacctgctgcccttcctgctcatgtgcttctgccactaccacatctgcaagacggtgcgc 1118
              |||||||| |||||||   |||||||||||||||||||| |||||||||| || || ||
Sbjct: 94318 tacctgcttcccttcgccctcatgtgcttctgccactacaacatctgcaaaacagtccgg 94259


Query: 1119  ctgtcggacgtgcgcgtgcggccggtgaacacctacgcgcgcgtgctgcgcttcttcagc 1178
              ||||||||  |  | |||||||||||| | ||| ||||||| | || |||||||| ||||
Sbjct: 94258 ctgtcggagatcagggtgcggccggtcaccacttacgcgcacctgttgcgcttctacagc 94199


Query: 1179  gaggtgcgcacggccaccaccgtcctcatcatgatcgtcttcgtcatctgctgctggggg 1238
              ||| ||||||| || |||||||| |||||||||| || |||  ||||| ||||||||||
Sbjct: 94198 gagatgcgcaccgcgaccaccgtgctcatcatgattgtgttcagcatcttctgctggggg 94139


Query: 1239  ccctactgc 1247
              |||||||||
Sbjct: 94138 ccctactgc 94130
```

>gi|6031165|ref|NM_001480.2| L U G Homo sapiens galanin receptor 1 (GALR1), mRNA
Length = 3056

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
||||||||||||| |||||||||| |||||||||
Sbjct: 1395 gctacctgctgccgctcctgctcatctgcttctgc 1429

>gi|24648696|ref|NM_169955.1| LU Drosophila melanogaster CG10823-PB [Drosophila m
(CG10823) mRNA, complete cds
Length = 1752

Score = 46.1 bits (23), Expect = 0.25
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1048 tggtggcctgctacctgctgccc 1070
|||||||||||||||||||||||
Sbjct: 1346 tggtggcctgctacctgctgccc 1368

>gi|24648694|ref|NM_142709.1| LU Drosophila melanogaster CG10823-PA [Drosophila m
(CG10823) mRNA, complete cds
Length = 4523

Score = 46.1 bits (23), Expect = 0.25
Identities = 23/23 (100%)
Strand = Plus / Plus

Query: 1048 tggtggcctgctacctgctgccc 1070
|||||||||||||||||||||||
Sbjct: 1346 tggtggcctgctacctgctgccc 1368

>gi|34895453|ref|NM_184181.1| U Oryza sativa (japonica cultivar-group) P0037C04.21
mRNA
Length = 1020

Score = 46.1 bits (23), Expect = 0.25
Identities = 29/31 (93%)
Strand = Plus / Minus

Query: 1196 caccgtcctcatcatgatcgtcttcgtcatc 1226
||||||||||||||| ||||||||||||
Sbjct: 991 caccgtcctcatcatcctcgtcttcgtcatc 961

>gi|33589379|gb|BT009988.1| Drosophila melanogaster RE47636 full insert cDNA
Length = 4808

```
 Score = 46.1 bits (23), Expect = 0.25
 Identities = 23/23 (100%)
 Strand = Plus / Plus


Query: 1048 tggtggcctgctacctgctgccc 1070
           |||||||||||||||||||||||
Sbjct: 1387 tggtggcctgctacctgctgccc 1409
```

>gi|14090356|dbj|AP003233.3| [D] Oryza sativa (japonica cultivar-group) genomic DNA, clone:P0037C04
Length = 137879

```
 Score = 46.1 bits (23), Expect = 0.25
 Identities = 29/31 (93%)
 Strand = Plus / Minus


Query: 1196  caccgtcctcatcatgatcgtcttcgtcatc 1226
              ||||||||||||||  ||||||||||||||
Sbjct: 73349 caccgtcctcatcatcctcgtcttcgtcatc 73319
```

>gi|21629409|gb|AC100863.2| [D] Homo sapiens chromosome 18, clone RP11-751H17, compl
Length = 175527

```
 Score = 46.1 bits (23), Expect = 0.25
 Identities = 32/35 (91%)
 Strand = Plus / Plus


Query: 1057   gctacctgctgcccttcctgctcatgtgcttctgc 1091
               |||||||||||||  |||||||||| |||||||||
Sbjct: 141358 gctacctgctgccgctcctgctcatctgcttctgc 141392
```

>gi|23171864|gb|AE003734.2| [L][D] Drosophila melanogaster chromosome 3R, section 72 complete sequence
Length = 241480

```
 Score = 46.1 bits (23), Expect = 0.25
 Identities = 23/23 (100%)
 Strand = Plus / Minus


Query: 1048  tggtggcctgctacctgctgccc 1070
              |||||||||||||||||||||||
Sbjct: 66542 tggtggcctgctacctgctgccc 66520
```

>gi|25140120|gb|AC096709.19| [D] Homo sapiens chromosome 18, clone RP11-707P24, comp
Length = 199285

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Minus

```
Query: 1057   gctacctgctgcccttcctgctcatgtgcttctgc 1091
              ||||||||||||  |||||||||| |||||||||
Sbjct: 154584 gctacctgctgccgctcctgctcatctgcttctgc 154550
```

>gi|17861010|gb|AC008308.8| Drosophila melanogaster, chromosome 3R, region 93C-9 BACR10M16, complete sequence
Length = 195868

Score = 46.1 bits (23), Expect = 0.25
Identities = 23/23 (100%)
Strand = Plus / Minus

```
Query: 1048   tggtggcctgctacctgctgccc 1070
              |||||||||||||||||||||||
Sbjct: 140664 tggtggcctgctacctgctgccc 140642
```

>gi|16258972|gb|AC008309.7| Drosophila melanogaster, chromosome 3R, region 93D-9 BACR06L13, complete sequence
Length = 162770

Score = 46.1 bits (23), Expect = 0.25
Identities = 23/23 (100%)
Strand = Plus / Minus

```
Query: 1048  tggtggcctgctacctgctgccc 1070
              |||||||||||||||||||||||
Sbjct: 26083 tggtggcctgctacctgctgccc 26061
```

>gi|44355566|gb|AY541036.1| Homo sapiens galanin receptor 1 mRNA, complete cds
Length = 1050

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Plus

```
Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
              ||||||||||||  |||||||||| |||||||||
Sbjct: 623  gctacctgctgccgctcctgctcatctgcttctgc 657
```

>gi|3064071|gb|U90658.1|HSGALNRS1 Homo sapiens galanin receptor (GALNR) gene, ex
Length = 1796

Score = 46.1 bits (23), Expect = 0.25

Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
||||||||||||| |||||||||| |||||||||
Sbjct: 1721 gctacctgctgccgctcctgctcatctgcttctgc 1755

>gi|1297337|gb|U53511.1|HSU53511 LU Homo sapiens galanin receptor (Gal1-R) mRNA,
Length = 1053

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
||||||||||||| |||||||||| |||||||||
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|775209|gb|U23854.1|HSU23854 LU Human galanin receptor mRNA, complete cds
Length = 1050

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
||||||||||||| |||||||||| |||||||||
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|559047|gb|L34339.1|HUMGALAREC LU Human galanin receptor mRNA, complete cds
Length = 1053

Score = 46.1 bits (23), Expect = 0.25
Identities = 32/35 (91%)
Strand = Plus / Plus

Query: 1057 gctacctgctgcccttcctgctcatgtgcttctgc 1091
||||||||||||| |||||||||| |||||||||
Sbjct: 623 gctacctgctgccgctcctgctcatctgcttctgc 657

>gi|12328514|dbj|AP002909.2| D Oryza sativa (japonica cultivar-group) genomic DNA,
clone:P0044F08
Length = 141528

Score = 46.1 bits (23), Expect = 0.25
Identities = 29/31 (93%)
Strand = Plus / Minus

```
Query: 1196  caccgtcctcatcatgatcgtcttcgtcatc 1226
             ||||||||||||||||  ||||||||||||||
Sbjct: 24919 caccgtcctcatcatcctcgtcttcgtcatc 24889
```

>gi|22296778|gb|AC121870.2| Mus musculus BAC clone RP24-121D5 from 9, complete s
Length = 191747

```
 Score = 44.1 bits (22), Expect = 0.98
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 114     cgctagcccccggccccgagcc 135
                ||||||||||||||||||||||
Sbjct: 162779 cgctagcccccggccccgagcc 162758
```

>gi|13677146|gb|AC013726.7| Homo sapiens BAC clone RP11-400N9 from 2, complete s
Length = 214647

```
 Score = 44.1 bits (22), Expect = 0.98
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 1059 tacctgctgcccttcctgctca 1080
               ||||||||||||||||||||||
Sbjct: 938  tacctgctgcccttcctgctca 959
```

>gi|29609103|dbj|AP005043.1| Streptomyces avermitilis genomic DNA, complete geno
Length = 299925

```
 Score = 44.1 bits (22), Expect = 0.98
 Identities = 22/22 (100%)
 Strand = Plus / Minus

Query: 305   ctccgcggccacggcggccgtg 326
              ||||||||||||||||||||||
Sbjct: 61594 ctccgcggccacggcggccgtg 61573
```

>gi|5001541|gb|AC005520.2|AC005520 Homo sapiens PAC clone RP5-1021I20 from 14q24
Length = 151123

```
 Score = 44.1 bits (22), Expect = 0.98
 Identities = 22/22 (100%)
 Strand = Plus / Plus

Query: 206   ggaggagccgcagccgccccgc 227
```

```
              ||||||||||||||||||||||
Sbjct: 28563 ggaggagccgcagccgccccgc 28584
```

>gi|21212029|emb|AL662811.20| D Mouse DNA sequence from clone RP23-202E24 on chrom
sequence
Length = 226642

Score = 44.1 bits (22), Expect = 0.98
Identities = 22/22 (100%)
Strand = Plus / Minus

```
Query: 1050  gtggcctgctacctgctgccct 1071
              ||||||||||||||||||||||
Sbjct: 37854 gtggcctgctacctgctgccct 37833
```

>gi|33457241|gb|AC127554.4| D Mus musculus BAC clone RP24-323K23 from chromosome 8
sequence
Length = 178416

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 719  gcctgccgccgccgcgggcc 739
             |||||||||||||||||||||
Sbjct: 6735 gcctgccgccgccgcgggcc 6715
```

>gi|21618432|gb|BC032702.1| L U G Homo sapiens G protein-coupled receptor 3, mRNA
IMAGE:5247608), complete cds
Length = 2145

Score = 42.1 bits (21), Expect = 3.9
Identities = 27/29 (93%)
Strand = Plus / Plus

```
Query: 1347 atcaaccctgtcatctacgccatccgcaa 1375
              ||||||||| |||||||||||| |||||||
Sbjct: 969  atcaaccctatcatctacgccttccgcaa 997
```

>gi|28630143|gb|AC124170.3| D Mus musculus BAC clone RP23-155H5 from 8, complete s
Length = 235023

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 719    gcctgccgccgccgcgggcc 739
```

```
              ||||||||||||||||||||
Sbjct: 224800 gcctgccgccgccgcggggcc 224780
```

>gi|38089509|ref|XM_357908.1| LU Mus musculus similar to SON protein (SON3) (Nega element-binding protein) (NRE-binding protein) (DBP-5) (Bax antagonist selected in saccharomyces 1) (BASS1) (LOC384869), mRNA
Length = 1047

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Plus

```
Query: 719 gcctgccgccgccgcggggcc 739
           ||||||||||||||||||||
Sbjct: 10  gcctgccgccgccgcggggcc 30
```

>gi|37533899|ref|NM_196270.1| U Oryza sativa (japonica cultivar-group) Centrin (OS mRNA
Length = 2565

Score = 42.1 bits (21), Expect = 3.9
Identities = 24/25 (96%)
Strand = Plus / Minus

```
Query: 749 cttctgcgccgccagccgcttcttc 773
           ||||||||||| ||||||||||||
Sbjct: 135 cttctgcgccgtcagccgcttcttc 111
```

>gi|23325376|gb|AE014636.1| D Bifidobacterium longum NCC2705 section 23 of 202 of genome
Length = 11431

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Plus

```
Query: 308  cgcggccacggcggccgtgct 328
           ||||||||||||||||||||
Sbjct: 7922 cgcggccacggcggccgtgct 7942
```

>gi|32567975|gb|AC105258.2| D Oryza sativa (japonica cultivar-group) chromosome 5 complete sequence
Length = 71145

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Plus

```
Query: 304   cctccgcggccacggcggccg 324
             ||||||||||||||||||||
Sbjct: 20100 cctccgcggccacggcggccg 20120
```

>gi|31431814|gb|AE017089.1| Oryza sativa (japonica cultivar-group) chromosome 10 of the complete sequence
Length = 300029

Score = 42.1 bits (21), Expect = 3.9
Identities = 24/25 (96%)
Strand = Plus / Plus

```
Query: 749   cttctgcgccgccagccgcttcttc 773
             |||||||||||| ||||||||||||
Sbjct: 67166 cttctgcgccgtcagccgcttcttc 67190
```

>gi|24418066|gb|AC009108.10| Homo sapiens chromosome 16 clone RP11-463O9, comple
Length = 168656

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Plus

```
Query: 719    gcctgccgccgccgcggggcc 739
              |||||||||||||||||||||
Sbjct: 134923 gcctgccgccgccgcggggcc 134943
```

>gi|44886087|dbj|AB164051.1| Oryzias latipes cGK I beta mRNA for cGMP-dependent pr beta, complete cds
Length = 2506

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 1198 ccgtcctcatcatgatcgtct 1218
             |||||||||||||||||||||
Sbjct: 891  ccgtcctcatcatgatcgtct 871
```

>gi|44886085|dbj|AB164050.1| Oryzias latipes cGK I alpha mRNA for cGMP-dependent p alpha, complete cds
Length = 2579

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 1198 ccgtcctcatcatgatcgtct 1218
           ||||||||||||||||||||
Sbjct: 964  ccgtcctcatcatgatcgtct 944
```

>gi|29366932|gb|AC009033.10| Homo sapiens chromosome 16 clone RP11-140I24, compl
Length = 158628

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Minus

```
Query: 682   ccttcctggacctcttcactc 702
              ||||||||||||||||||||
Sbjct: 72712 ccttcctggacctcttcactc 72692
```

>gi|13424739|gb|AE005972.1| Caulobacter crescentus CB15 section 298 of 359 of th
Length = 11923

Score = 42.1 bits (21), Expect = 3.9
Identities = 21/21 (100%)
Strand = Plus / Plus

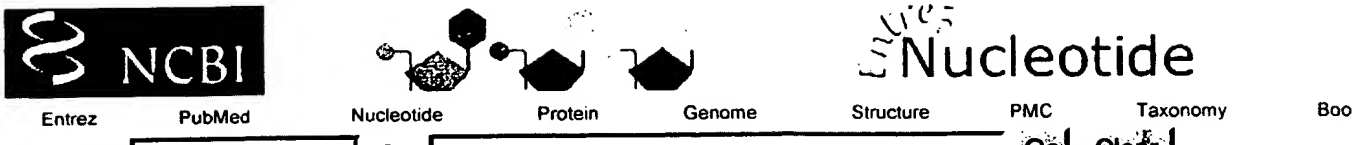
```
Query: 1251 ctggtgctgctggccgccgcc 1271
           ||||||||||||||||||||
Sbjct: 6287 ctggtgctgctggccgccgcc 6307
```

```
Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31

Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 14,905,373
Number of Sequences: 2102977
Number of extensions: 5816
Number of successful extensions: 19
Number of sequences better than 10.0: 0
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 18
length of query: 1860
length of database: 10,130,642,339
A: 0
X1: 11 (20.0 bits)
X2: 15 (30.0 bits)
X3: 25 (50.0 bits)
```

S1: 12 (25.0 bits)



1: M76676. Homo sapiens leuk...[gi:2810988]

```
LOCUS       HUMNPIIY20              1481 bp    mRNA    linear   PRI 27-JAN-1998
DEFINITION  Homo sapiens leukocyte platelet-activating factor receptor mRNA,
            complete cds.
ACCESSION   M76676
VERSION     M76676.1  GI:2810988
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1481)
  AUTHORS   Kunz,D., Gerard,N.P. and Gerard,C.
  TITLE     The human leukocyte platelet-activating factor receptor. cDNA
            cloning, cell surface expression, and construction of a novel
            epitope-bearing analog
  JOURNAL   J. Biol. Chem. 267 (13), 9101-9106 (1992)
  MEDLINE   92250505
   PUBMED   1374385
COMMENT     On Jan 27, 1998 this sequence version replaced gi:189269.
FEATURES             Location/Qualifiers
     source          1..1481
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="U937, cAMP induced"
                     /cell_type="leukocyte"
     CDS             89..1057
                     /note="putative"
                     /codon_start=1
                     /product="leukocyte platelet-activating factor receptor"
                     /protein_id="AAB97766.1"
                     /db_xref="GI:189270"
                     /translation="MALLGSQHSGAPSAAGPPGGTSSAATAAVLSFSTVATAALGNLS
                     DASGGGTAAAPGGGGLGGSGAAREAGAAVRRPLGPEAAPLLSHGAAVAAQALVLLLIF
                     LLSSLGNCAVMGVIVKHRQLRTVTNAFILSLSLSDLLTALLCLPAAFLDLFTPPGGSA
                     PALPAGPWRGFCRPSRFFSSCFGIVYAQRGAHLVGPLLRYRRPPREKIGRRRALQLLA
                     GAWLTALGFSLPWELLGAPRELAAGQSFHGCLYRTSPDPAQLGGPFSVGLVVACYLLP
                     FLLICFCHYHICKTVRLSDVRVRPVNTYARVLRSSARCARPPPSSS"
ORIGIN
        1 ggccgccgcc cccggtgcgg gatgaggaga tccgcggccg ccactgggcc ccatggagga
       61 gccgccgccg ccccgcccac cagcgagcat ggccttactg ggcagccagc actccggcgc
      121 cccctccgcg gccggcccac ctggcgggac ttcctcagcg gccacggcgg ccgtgctctc
      181 cttcagcacc gtggcgaccg cggcgctggg gaacctgagc gacgcaagcg gaggcggcac
      241 agctgccgct cccggtggcg gcggccttgg cgggtccggg gcagcgcggg aggcgggggc
      301 ggcggtgagg cggccgctag gcccggaggc ggcgccgctg ctgtcgcacg gagctgcagt
      361 ggcggcccag gcgctcgtcc tcctgctcat cttcctgctg tctagccttg gcaactgcgc
      421 ggtgatgggg gtgattgtga agcaccggca gctccgcacc gtcaccaacg ccttcatcct
      481 gtcgctgtcc ctatcggatc tgctcacggc gctgctctgc ctgcccgccg ccttcctgga
      541 cctcttcact ccgcccgggg gttcggcgcc tgcgctgccc gcggggccct ggcgcggctt
```

```
 601 ctgccggcca agccgcttct tcagctcgtg cttcggcatc gtgtacgctc agcgtggcgc
 661 tcatctcgtt ggaccgttac tgcgctatcg tcggccgccg cgggagaaga tcggccgccg
 721 ccgcgcgctg cagctgctgg cgggcgcctg gctgacggcc ctgggcttct ccttgccctg
 781 ggagctgctc ggggcgcccc gggaactcgc ggcgggccag agcttccacg gctgcctcta
 841 ccggacctcc ccggaccccg cgcagctggg cggccccttc agcgtggggc tggtggtggc
 901 ctgctacctg ctgcccttcc tgctcatctg cttctgccac taccacatct gcaagacggt
 961 gcgcctgtcg gacgtgcgcg tgcggccggt gaacacctac gcgcgcgtgc tgcgttcttc
1021 agcgaggtgc gcacggccac caccgtcctc atcatgatcg tcttcgtcat ctgctgctgg
1081 gggccctact gcttcctggt gctgctggcc gccgcccggc aggcccagac catgcaggcc
1141 ccctcgctcc tcagcgtggt ggccgtctgg ctgacctggg ccaatggggc catcaaccct
1201 gtcatctacg ccatccgcaa tcccaacatt tcgatgctcc tagggcgcaa ccgcgaggag
1261 ggctaccgga ctaggaatgt ggacgctttc ctgcccagcc agggcccggg tctgcaagcc
1321 agaagccgca gtcgccttcg aaaccgctat gccaaccggc tgggggcctg caacaggatg
1381 tcctcttcca acccggccag cggagtggca ggggacgtgg ccatgtgggc cgcaaaaatc
1441 cagttgtact tttctgccga gaggaccacc agagccggtg a
//
```


Mar 11 2004 07:26:05

Entrez Nucleotide

1: AY255588. Homo sapiens leuk...[gi:29611577]

```
LOCUS       AY255588                546 bp    mRNA    linear   PRI 08-APR-2003
DEFINITION  Homo sapiens leukocyte platelet-activating factor receptor mRNA,
            partial cds.
ACCESSION   AY255588
VERSION     AY255588.1  GI:29611577
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,
            Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,
            Bergmann,J.E. and Gaitanaris,G.A.
  TITLE     The G Protein-Coupled Receptor Repertoires of Human and Mouse
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (8), 4903-4908 (2003)
REFERENCE   2  (bases 1 to 546)
  AUTHORS   Vassilatis,D.K., Hohmann,J.G., Zeng,H., Li,F., Ranchalis,J.E.,
            Mortrud,M.T., Brown,A., Rodriguez,S.S., Weller,J.R., Wright,A.C.,
            Bergmann,J.E. and Gaitanaris,G.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2003) Primal, Inc., 1124 Columbia Street,
            Seattle, WA 98104, USA
FEATURES             Location/Qualifiers
     source          1..546
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     CDS             <1..>546
                     /note="G protein-coupled receptor; HUMNPIIY20"
                     /codon_start=1
                     /product="leukocyte platelet-activating factor receptor"
                     /protein_id="AAO85100.1"
                     /db_xref="GI:29611578"
                     /translation="HGAAVAAQALVLLLIFLLSSLGNCAVMGVIVKHRQLRTVTNAFI
                     LSLSLSDLLTALLCLPAAFLDLFTPPGGSAPAAAAGPWRGFCAASRFFSSCFGIVSTL
                     SVALISLDRYCAIVRPPREKIGRRRALQLLAGAWLTALGFSLPWELLGAPRELAAAQS
                     FHGCLYRTSPDPAQLGAAFSVG"
ORIGIN
        1 cacggagctg cagtggcggc ccaggcgctc gtcctcctgc tcatcttcct gctgtctagc
       61 cttggcaact gcgcggtgat gggggtgatt gtgaagcacc ggcagctccg caccgtcacc
      121 aacgccttca tcctgtcgct gtccctatcg gatctgctca cggcgctgct ctgcctgccc
      181 gccgccttcc tggacctctt cactccgccc gggggttcgg cgcctgccgc cgccgcgggg
      241 ccctggcgcg gcttctgcgc cgccagccgc ttcttcagct cgtgcttcgg catcgtgtcc
      301 acgctcagcg tggcgctcat ctcgttggac cgttactgcg ctatcgtgcg gccgccgcgg
      361 gagaagatcg gccgccgccg cgcgctgcag ctgctggcgg gcgcctggct gacggccctg
      421 ggcttctcct tgccctggga gctgctcggg gcgccccggg aactcgcggc ggcgcagagc
      481 ttccacggct gcctctaccg gacctccccg gaccccgcgc agctgggcgc ggccttcagc
      541 gtgggg
```

//

Mar 11 2004 07:26:05

Entrez Nucleotide

1: NM_022571. Homo sapiens G pr...[gi:32261308]

LOCUS NM_022571 1485 bp mRNA linear PRI 23-DEC-2003
DEFINITION Homo sapiens G protein-coupled receptor 135 (GPR135), mRNA.
ACCESSION NM_022571
VERSION NM_022571.3 GI:32261308
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1485)
AUTHORS Fredriksson,R., Hoglund,P.J., Gloriam,D.E., Lagerstrom,M.C. and Schioth,H.B.
TITLE Seven evolutionarily conserved human rhodopsin G protein-coupled receptors lacking close relatives
JOURNAL FEBS Lett. 554 (3), 381-388 (2003)
PUBMED 14623098
REFERENCE 2 (bases 1 to 1485)
AUTHORS Kunz,D., Gerard,N.P. and Gerard,C.
TITLE The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and construction of a novel epitope-bearing analog
JOURNAL J. Biol. Chem. 267 (13), 9101-9106 (1992)
PUBMED 1374385
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AY288418.1.
On Jun 26, 2003 this sequence version replaced gi:24475665.
FEATURES Location/Qualifiers
source 1..1485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q23.1"
gene 1..1485
/gene="GPR135"
/note="synonyms: PAFR, HUMNPIIY20"
/db_xref="GeneID:64582"
/db_xref="LocusID:64582"
/db_xref="MIM:607970"
CDS 1..1485
/gene="GPR135"
/note="platelet-activating factor receptor;
go_component: integral to membrane [goid 0016021] [evidence IEA];
go_function: platelet activating factor receptor activity [goid 0004992] [evidence TAS] [pmid 1374385];
go_function: receptor activity [goid 0004872] [evidence IEA];
go_process: G-protein coupled receptor protein signaling

```
                     pathway [goid 0007186] [evidence IEA];
                     go_process: biological_process unknown [goid 0000004]
                     [evidence ND] [pmid 1374385]"
                     /codon_start=1
                     /product="putative leukocyte platelet-activating factor
                     receptor"
                     /protein_id="NP_072093.2"
                     /db_xref="GI:32261309"
                     /db_xref="GeneID:64582"
                     /db_xref="LocusID:64582"
                     /db_xref="MIM:607970"
                     /translation="MEEPQPPRPPASMALLGSQHSGAPSAAGPPGGTSSAATAAVLSF
                     STVATAALGNLSDASGGGTAAAPGGGGLGGSGAAREAGAAVRRPLGPEAAPLLSHGAA
                     VAAQALVLLLIFLLSSLGNCAVMGVIVKHRQLRTVTNAFILSLSLSDLLTALLCLPAA
                     FLDLFTPPGGSAPAAAAGPWRGFCAASRFFSSCFGIVSTLSVALISLDRYCAIVRPPR
                     EKIGRRRALQLLAGAWLTALGFSLPWELLGAPRELAAAQSFHGCLYRTSPDPAQLGAA
                     FSVGLVVACYLLPFLLMCFCHYHICKTVRLSDVRVRPVNTYARVLRFFSEVRTATTVL
                     IMIVFVICCWGPYCFLVLLAAARQAQTMQAPSLLSVVAVWLTWANGAINPVIYAIRNP
                     NISMLLGRNREEGYRTRNVDAFLPSQGPGLQARSRSRLRNRYANRLGACNRMSSSNPA
                     SGVAGDVAMWARKNPVVLFCREGPPEPVTAVTKQPKSEAGDTSL"
misc_feature         358..1161
                     /gene="GPR135"
                     /note="7tm_1; Region: 7 transmembrane receptor (rhodopsin
                     family)"
                     /db_xref="CDD:5814"
misc_feature         <976..1230
                     /gene="GPR135"
                     /note="KOG4220; Region: Muscarinic acetylcholine receptor
                     [Signal transduction mechanisms]"
                     /db_xref="CDD:21996"
variation            complement(14)
                     /replace="T"
                     /replace="G"
                     /db_xref="dbSNP:1752428"
variation            105
                     /gene="GPR135"
                     /replace="C"
                     /replace="A"
                     /db_xref="dbSNP:3742645"
variation            248
                     /gene="GPR135"
                     /replace="T"
                     /replace="C"
                     /db_xref="dbSNP:3742646"
variation            complement(1442)
                     /replace="G"
                     /replace="A"
                     /db_xref="dbSNP:1752427"
ORIGIN
        1 atggaggagc cgcagccgcc ccgcccacca gcgagcatgg ccttactggg cagccagcac
       61 tccggcgccc cctccgcggc cggcccacct ggcgggactt cctccgcggc cacggcggcc
      121 gtgctctcct tcagcaccgt ggcgaccgcg gcgctgggga acctgagcga cgcaagcgga
      181 ggcggcacag ctgccgctcc cggtggcggc ggccttggcg ggtccggggc agcgcgggag
      241 gcgggggcgg cggtgaggcg gccgctaggc ccggaggcgg cgccgctgct gtcgcacgga
      301 gctgcagtgg cggcccaggc gctcgtcctc ctgctcatct tcctgctgtc tagccttggc
      361 aactgcgcgg tgatgggggt gattgtgaag caccggcagc tccgcaccgt caccaacgcc
      421 ttcatcctgt cgctgtccct atcggatctg ctcacggcgc tgctctgcct gcccgccgcc
      481 ttcctggacc tcttcactcc gcccgggggt tcggcgcctg ccgccgccgc ggggccctgg
      541 cgcggcttct gcgccgccag ccgcttcttc agctcgtgct tcggcatcgt gtccacgctc
      601 agcgtggcgc tcatctcgtt ggaccgttac tgcgctatcg tgcggccgcc gcgggagaag
```

```
   661 atcggccgcc gccgcgcgct gcagctgctg gcgggcgcct ggctgacggc cctgggcttc
   721 tccttgccct gggagctgct cggggcgccc cgggaactcg cggcggcgca gagcttccac
   781 ggctgcctct accggacctc cccggacccc gcgcagctgg gcgcggcctt cagcgtgggg
   841 ctggtggtgg cctgctacct gctgcccttc ctgctcatgt gcttctgcca ctaccacatc
   901 tgcaagacgg tgcgcctgtc ggacgtgcgc gtgcggccgg tgaacaccta cgcgcgcgtg
   961 ctgcgcttct tcagcgaggt gcgcacggcc accaccgtcc tcatcatgat cgtcttcgtc
  1021 atctgctgct gggggcccta ctgcttcctg gtgctgctgg ccgccgcccg gcaggcccag
  1081 accatgcagg ccccctcgct cctcagcgtg gtggccgtct ggctgacctg ggccaatggg
  1141 gccatcaacc ctgtcatcta cgccatccgc aatcccaaca tttcgatgct cctagggcgc
  1201 aaccgcgagg agggctaccg gactaggaat gtggacgctt tcctgcccag ccagggcccg
  1261 ggtctgcaag ccagaagccg cagtcgcctt cgaaaccgct atgccaaccg gctgggggcc
  1321 tgcaacagga tgtcctcttc caacccggcc agcggagtgg caggggacgt ggccatgtgg
  1381 gcccgcaaaa atccagttgt acttttctgc cgagagggac caccagagcc ggtgacggca
  1441 gtgaccaaac agcctaaatc cgaagctggg gataccagcc tctaa
//
```


Mar 11 2004 07:26:05

Home

Features
- What sets our kits apart?
- COX-3 News
- PGE2-FPIA

PRIONS

Products
- Product Lines
- Advanced Product Search
- New Products
- Assay Kits
- Promotional Products
- Cayman Challenge
- Analysis Tools
- Assay Service

Corporate Info
- Company Profile
- Conferences
- Employment
- Favorite Links

Literature Request
- New Product Update
- Print Catalog
- Poster Request
- Scientific Illustrations

Contact Us
- Customer Service
- Technical FAQ
- Technical Services
- Distributors
- Funds Request
- Website Feedback

Other
- Site Map
- Browser Recommendation
- Order Terms
- Privacy Statement

1180 East Ellsworth Road
Ann Arbor, Michigan 48108

160600 PAF Receptor (human) Monoclonal Antibody

Data | Description | Related Products

below for pricing and ordering.

Antigen: human amino acids 260-269 (LGFQDSKFHQ)[1 2 3] · Host: mouse · Cross-reactivity: (+) human, bovine, and porcine PAF receptor · Applications: flow cytometry, immunocytochemistry; may not work for Western blot · IgG2a · Clone designation: 11A4 (clone 21) · PAF is a potent phospholipid mediator which exerts diverse biological actions by interaction with a G protein-coupled PAF receptor. The PAF receptor has been cloned from a number of species including human, rat, and guinea pig and is

SEARCH
Search for products using a keyword, CAS number, or Cayman catalog number.

SEARCH

Other resources
- MSDSs
- Distributors
- Order Terms
- Printed Catalog

ORDER
Enter the catalog numbers of products you wish to add to your shopping cart.

GO

LOGIN
email

password

LOGIN

REGISTER
New to Cayman?
Click here to discover the benefits of becoming a registered user.

REGISTER

SHOPPING CART
Your shopping cart is empty.

VIEW

NEW PRODUCT IDEAS
Do you have any new product ideas?

SUGGEST

RECENTLY BROWSED
in catalog number order
- PAF Receptor (human) Monoclonal Antibody

Ann Arbor, Michigan 48108
USA

toll free 800.364.9897
direct dial 734.971.3335

protein coupled PAF receptor. The PAF receptor has been cloned from a number of species including human, rat, and guinea pig and is characterized as a 7-transmembrane receptor which induces phosphoinositol turnover through G-protein coupling.[1 2 3 4 5] Northern blot analysis reveals that the receptor is expressed in leukocytes, placenta, lung, spleen, small intestine, kidney, liver, and brain.[3 4] In leukocyte cell populations the receptor is found on platelets, myocytes, neutrophils, and B-cells, whereas resting T-cells and natural killer cell lines do not express the PAF receptor.[6] Human monocytes treated with INF-γ have a 2-6 fold increase in PAF receptor expression compared to untreated cells.[7]

1 Nakamura, M., Honda, Z.,

Izumi, T., et al. Molecular cloning and expression of platelet-activating factor receptor from human leukocytes. J. Biol. Chem. 266, 20400-20405 (1991).

[2] Kunz, D., Gerard, N.P., and Gerard, C. The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and construction of a novel epitope-bearing analog. J. Biol. Chem. 267, 9101-9106 (1992).

[3] Ye, R.D., Prossnitz, E.R., Zou, A., et al. Characterization of a human cDNA that encodes a functional receptor for platelet activating factor. Biochem. Biophys. Res. Commun. 180, 105-111 (1991).

[4] Bito, H., Honda, Z., Nakamura, M., et al. Cloning, expression and tissue distribution of rat platelet-activating-factor-receptor cDNA. Eur. J. Biochem. 227, 211-218 (1994).

[5] Honda, Z., Nakamura, M., Miki, I., et al. Cloning by functional expression of platelet-activating factor receptor from guinea-pig lung. Nature 349, 342-346 (1991).

[6] Müller, E., Dagenais, P.,

Alami, N., et al. Identification and functional characterization of platelet-activating factor receptors in human leukocyte populations using polyclonal anti-peptide antibody. Proc. Natl. Acad. Sci. USA 90, 5818-5822 (1993).

7 Quellet, S., Müller, E., and Rola-Pleszczynski, M. IFN-γ up-regulates platelet-activating factor receptor gene expression in human monocytes. J. Immunol. 152, 5092-5099 (1994).

General References

There are no general references associated with this product.

Download Product Insert
126 Kb PDF

Download Material Safety Data Sheet (MSDS) 8 Kb PDF

Printer-friendly

version of this page small PDF (usually less than 100 Kb)

- US Letter paper 8½" × 11"
- A4 paper 21cm × 29.7cm

Pricing Information

Pricing is for North America only. Other customers should contact a distributor in their region.

*This product is also available in **bulk** quantities. Please contact our Sales*

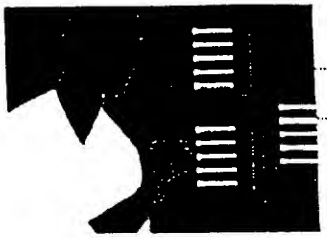
Department
<sales@caymanchem.com>
for
a
quote.

Item
total
$0.00 •
Shopping
cart
total
$0.00

Size	Price	Quantity
Pricing updated 2004-03-16		
1 ea	$150.00	

Update and View Cart

Invitrogen™
life technologies



Invitrogen Clones

- Invitrogen Clones
- Search Clones
  - CloneRanger™
  - Ultimate™ ORF Browser
  - Important Gene Families
- Clone Collections
  - Ultimate™ ORF Clones
  - Genestorm® Clones
  - Full-Length Clones
  - EST Clones
  - BAC/PAC Clones

Online Catalog - Invitrogen Clones

Ultimate™ ORF Browser:

Advanced Search for Ultimate™ ORF Clones

Search By ID or Keyword | Search By Sequence | Browse By Gene Ontology

33 total records for G-Protein Coupled Receptors

Buy	Clone ID	Species	Definition	Gene Symbol
☐	IOH3294	Human	complement component 5 receptor 1 (C5a ligand); complement component-5 receptor-2 (C5a ligand)	C5R1
☐	IOH12614	Human	purinergic receptor P2Y, G-protein coupled, 11	P2RY11
☐	IOH22483	Human	clone MGC:33224 IMAGE:5267661, mRNA, complete cds.	RDC1
☐	IOH14039	Human	Similar to putative nuclear protein ORF1-FL49	ORF1-FL49
☐	IOH11484	Human	glycoprotein Ib (platelet), alpha polypeptide	GP1BA
☐	IOH1987	Human	tachykinin receptor 1 isoform short; NK-1 receptor; Tachykinin receptor 1 (substance P receptor; neurokinin-1 receptor); tachykinin 1 receptor (substance P receptor, neurokinin 1 receptor); neurokinin 1 receptor	TACR1
☐	IOH13056	Human	similar to POSSIBLE GUSTATORY RECEPTOR CLONE PTE01	LOC11513:
☐	IOH9916	Human	coagulation factor II (thrombin) receptor-like 1	F2RL1
☐	IOH9624	Human	vasoactive intestinal peptide receptor 2	VIPR2
☐	IOH10679	Human	endothelin receptor type A	EDNRA
☐	IOH22637	Human	Similar to parathyroid hormone receptor 1, clone MGC:34562 IMAGE:5180885, mRNA, complete cds.	PTHR1
☐	IOH13583	Human	Duffy blood group	FY
☐	IOH4585	Human	cholecystokinin B receptor	CCKBR
☐	IOH11033	Human	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4; G protein-coupled receptor; LPA receptor EDG4; Lysophosphatidic acid receptor EDG4	EDG4
☐	IOH10866	Human	CD97 antigen isoform 2 precursor; leukocyte antigen CD97; seven-span transmembrane protein	CD97
☐	IOH22632	Human	formyl peptide receptor-like 1; lipoxin A4 receptor (formyl peptide receptor related)	FPRL1
☐	IOH22649	Human	adrenomedullin receptor	ADMR
☐	IOH13239	Human	super conserved receptor expressed in brain 3	SREB3

Customer Service: 1800 786 1236
Technical Support: 318 219 1123
Fax: 318 798 1849
Info@fabgennix.com
www.fabgennix.com

FabGennix Inc.
INTERNATIONAL

New Item

Novel Orphan retinal G-protein coupled Receptor (GPCR-75) selective antibodies

Anti-GPCR-75Antibodies (GPCR75-100P, GPCR75-101AP and GPCR75-112AP)

Recently a novel human G-protein coupled receptor gene has been characterized and mapped to chromosome 2p16. This gene codes for a 540 amino acid protein in retinal pigment epithelium (RPE) and cells surrounding retinal arterioles. In contrast, the Northern blot data obtained from mouse sections suggest the expression of transcripts in photoreceptor inner segments and I outer plexiform layer. The transcripts of the GPCR-75 gene (7kb) are also found in abundance in brain sections. So far, no mutations in GPCR-75 protein were identified in patients suffering from Doyne's honeycomb retinal dystrophy (DHRD), an inherited retinal degeneration disease that maps to chromosome 2p16 (1).

The GPCR-75 protein is approximately 78 kDa (540 amino acids) protein that is primarily expressed in human retinal pigment epithelium (RPEs). The GPCR-75 sequence analyses suggest the presence of 7 trans-membrane domains, a characteristic feature of GPCR. The protein has putative N-glycosylation sites near the extra cellular N-terminal end of the proteins. The protein has a large 3 intra cellular loop which might be the site for interaction of G-proteins. The short carboxy terminal is intracellular and has putative post-translational modification lipid modification sites.

The Anti-GPCR-75-selective antibodies were generated against conserved sequences near N- and C-termini of the protein that are unique to GPCR-75 protein. The polyclonal antibody strongly labels a 78 kDa protein in RPE cell extracts. Anti-GPCR-75-selective antibody is also available in affinity-purified form for confocal, Western blotting and immunocytochemical analyses. *FabGennix Int. Inc.* will also conjugate antibodies with fluorescent probes upon request at extra charge. *FabGennix Int. Inc.* will also provides antibodies against proteins that are involved in retinal degenerative diseases such as various Anti-PDE antibodies, Anti-MERTK, Anti-Phospho-MERTK, EGF-containing fibulin like intracellular protein (EFEMP1), Anti-Myocilin (TIGR), Anti-Bestrophin, Anti-ELVOL4 and a Usher syndrome specific Anti-USH2a antibodies etc. FabGennix Int. Inc employs cyclic peptide methodology for generating antibodies, which results in higher titer and specificity (2). FabGennix Int. Inc., will also provide Western blot positive controls for most of these antibodies in ready-to-use buffer for easy identification of respective proteins. Limited quantities of antigens are also available. Please enquire for their availability before ordering.

Catalog #	Host Species	Nature	Cross reactivity	Quantity	volume	Price
GPCR75-100P	Rabbit	Polyclonal antisera	R, M, H	100 ml	100 ul	$ 195.00
GPCR75-101AP	Rabbit	Affinity purified IgG	R, M, H	100 ug	150 ul	$ 225.00
GPCR75-112AP	Rabbit	Affinity purified IgG	R, M, H	100 ug	150 ul	$ 225.00
PC-GPCR75	N/A	WB positive control	Rat	For 5 App	60 ul	$ 75.00
P-GPCR75	N/A	Antigenic peptides	n/a	250 ug	Inquire	$ 65.00

R = rat; M = mouse; H = human; C = chicken; monk = monkey ; * not all variants are labeled equally

Immunogen: Synthetic cyclic peptide (GPCR75-101AP = PNATSLHVPHSQEGNSTS-amide; GPCR75-112AP = STSLQEGLQDLIHTATLVTC-amide).

Concentration: GPCR75-101AP, GPCR-112AP IgG concentration 0.75-1.25 mg/ml in 50% antibody stabilization buffer.

Applications: Antibody GPCR75-100/GPCR75-101AP are ideal for WB, IMM and IHC assays. The dilutions for this antibody is for reference only, Investigators are expected to determine the optimal conditions for specific assay in his/her laboratory. Dilutions: WB > 1:500; Immunoprecipitation & Lp pull-down assays> 1:250

Reactivity: This antibody detects a single 78 kDa Orphan GPCR75 protein in human RPE cell extracts.

Protocols: Standard protocol for various applications (WB; IMM and IHC) of this antibody is provided with the product specification sheet, however, FabGennix Int. Inc. strongly recommends investigators to optimize conditions for use of this antibody in their laboratories.

Form/Storage: The antiserum is supplied in antibody stabilization buffer with 0.02% sodium azide or thimerosal/merthiolate as preservative. The affinity-purified antibodies are purified on antigen-epoharose affinity column and supplied as 1-1.25 mg/ml IgG in antibody stabilization buffer containing preservatives with low viscosity and cryogenic properties. For long-term storage of antibodies, store at -20°C. Now these antibodies can be stored at -20°C and used immediately with out thawing. FabGennix Inc. does not recommend storage of very dilute antibody solutions unless they are prepared in specially formulated multi use antibody dilution buffer (Cat # DiluOBuffer). Working solutions of antibodies in DiluOBuffer should be filtered through 0.45µ filter after every use for long-term storage.

78 kDa Orphan Receptor-75 in human RPE cells. Antibody GPCR-100P (1:400)

References:

1. Turticlin B. E., Krischner L. S., Bellingham J., Baffi. J. Taymanas S. E., Gregor E. K., Cosky K., Stratakis C. A., Gregory-Evans C. Y. Biochem. Biophys. Res. Commun. 260, 174-180, 1999.
2. Farooqui, S. M., Brock. W. J., A. Hamdi., Prasad. C. (1991) J. Neurochem. 57, 1363-1369.

• For users who may require large amounts of GPCR75-100P or GPCR75-101AP, please enquire about bulk material discounts.
This Product is for Research Use Only and is NOT intended for use in humans or clinical diagnosis.

061901-0020SF1001Z-rev10.00

FabGennix Inc.
INTERNATIONAL
2940 Youree Drive, Suite E, Shreveport, LA 71104

生工有限公司

Rat Taste Receptor 2 (TR2) Antibodies

Rat Taste Receptor 2 (TR2) Antibodies

Cat. # TR21-P, Rat TR2 Control Peptide # 1, SIZE: 100 ug/100 ul
FORM: Œ Soln Œ Lyophilized Lot # 3113P

Cat. # TR21-S, Rabbit Anti-rat TR2 antiserum # 1, SIZE: 100 ul neat antiserum
FORM: Œ Soln Œ Lyophilized. Lot # 38889S

Cat. # TR21-A, Rabbit Anti-rat TR2 Ab # 1 (affinity pure) SIZE: 100 ug
FORM: Œ Soln Œ Lyophilized. Lot # 38889A

Higher vertebrates are believed to possess at least five basic tastes: Sweet, bitter, sour, salty, and unami (the taste of monosodium glutamate). Taste receptor cells that may selectively reside in various parts of the tongue and respond to different tastants and perceive these taste modalities. Circumvallate papillae, found at the very back of the tongue, are particularly sensitive to biter substances. Foliate papillae, found at the posterior lateral edge of the tongue, are sensitive to sour and bitter. Fungiform papillae at the front of the tongue specialize in sweet taste.

Recently, two novel taste receptors, TR1 and TR2, have been cloned with distinct topographical distribution in taste receptor cells and taste buds. TRs are members of a new group of 7 TM domain containing GPCR distantly related to other chemosensory receptors (Ca+-sensing receptor (CaSR, a family of putative hormone receptor (V2R), and metabotropic glutamate receptors). TR1 is expressed in all fungiform taste buds, whereas TR2 localized to the circumvallate taste buds. Both receptors do not co-localize with gustducin.

Source of Antigen and Antibodies

TR1 (rat 840 aa) and TR2 (rat 843 aa) share ~40% homology with each other, and ~30% with CaSR, and 22-30% with V2R pheromone receptors and mGLURs. Rat TR are 7 TM domain containing protein with an extra long N-terminal, extracellular domain (1). A 19 AA Peptide (designated TR21-P; control peptide) sequence near the C-terminus of rat TR2(1) was selected for antibody production. The peptide was coupled to KLH, and antibodies generated in rabbits. Antibody has been affinity purified using control peptide-Sepharose.

Form & Storage

Control peptide Solution is provided in PBS, pH 7.4 at 1 mg/ml (100 ug/100 ul). Antiserum is supplied as neat serum (100 ul soln or lyophilized). Affinity pure antibodies were purified over the peptide-Sepharose column and supplied as 1 mg/ml soln in PBS, pH 7.4 and 0.1% BSA as stabilizer (100 ul in solution or Lyophilized).
The peptides and antibodies also contain 0.1% sodium azide as preservative. Lyophilized products should be reconstituted in 100 ul water and gently mixed for 15 min at room temp. All peptide/antibody

received in solution or

reconstituted from lyophilized vials should be stored frozen at -20oC or below in suitable aliquots. It is not recommended to store diluted solutions. Avoid repeated freeze and thaw.

Recommended Usage

Western Blotting (1:1K-5K for neat serum and 1-10 ug/ml for affinity pure antibody using ECL technique).

ELISA: Control peptide can be used to coat ELISA plates at 1 ug/ml and detected with antibodies (1:10-50K for neat serum and 0.5-1 ug/ml for affinity pure).

Histochemistry & Immunofluorescence: We recommend the use of affinity purified antibody at 1-20 ug/ml in paraformaldehyde fixed sections of tissues (1).

Specificity & Cross-reactivity

The 19 AA rat TR21-P control peptide is specific for rat TR2. It has no significant sequence homology with TR1 or gustducin or pheromone receptors. Antibody cross-reactivity in various species has not been studied. The TR21-P control peptide is available to confirm specificity of antibodies.

References:

1. Hoon MA et al (1999) Cell 96, 541-555; Lindemann B (1999) Nature Med. 5, 381-382

"Neat Antisera" are the unpurified antiserum and it is suitable for ELISA and Western.
"Affinity pure" antibodies have been over the antigen-affinity column and recommended for immunohistochemical applications.
"Control peptides" can not be used for Western as they are very short peptides. They are intended for ELISA or antibody competition studies.

List of Related Products

回頁首回 回首頁回

生工有限公司
MDBio, Inc.
全省免付費服務專線：0800-072-222 | 電話：(02)27474876 | 傳真：(02)28238024
網站：www.mdbio.com.tw | 電子郵件：mdbio@mdbio.com.tw

中華民國92年06月09日更新